Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # :_____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

STAFF USE ONLY

Searcher: D. Schreiber
Searcher Phone #: 272-2522
Searcher Location: Remsen E01 A61
Date Searcher Picked Up: ~~4/15~~
Date Completed: 4/15
Searcher Prep & Review Time: 12
Clerical Prep Time: _____
Online Time: 92

Type of Search

NA Sequence (#) 21
AA Sequence (#) _____
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr.Link _____
Lexis/Nexis _____
Sequence Systems Compugen
WWW/Internet _____
Other (specify) _____

PTO-1590 (8-01)

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 119583

TO: Terra Gibbs **Location: rem/2d10/2c18** **Art Unit: 1635** **Friday, April 16, 2004** **Case Serial Number: 09/954556**	**From: David Schreiber** **Location: Biotech-Chem Library** **Remsen E01A61** **Phone: 272-2526** **david.schreiber@uspto.gov**

Search Notes

STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact***:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

  Types of relevant prior art found:
  - ☐ Foreign Patent(s)
  - ☐ Non-Patent Literature
    (journal articles, conference proceedings, new product announcements etc.)
- *Relevant prior art **not found**:*
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.

Schreiber, David

1 119583

From: Gibbs, Terra
Sent: Wednesday, March 31, 2004 4:20 PM
To: Schreiber, David
Subject: Sequence searcj request...

Hi David,
I have another request for a score over length search:
I need a length limited nucleotide sequence search against nucleobases 1479 through 1508 of SEQ ID NO:3 in USSN 09,954,556, where the returns are rank ordered based on the score over length/ratio as we've discussed. I need the lengths limited to hits between 8 and 50 nucleotides, and I'll take as many hits as you can import into excel (64,000?), and alignments for anything above .75 on the above ratio. Hope this is clear, please call me if it's not. I also need the interference databases searched if possible.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
571-272-0758

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:33:22 ; Search time 0.001 Seconds
(without alignments)
79.200 Million cell updates/sec

Title: us-09-954-556-3
Perfect score: 30
Sequence: 1 cacgaccaagaagccagacttcagcagcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 102 seqs, 1320 residues

Total number of hits satisfying chosen parameters: 204

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 102 summaries

Database : rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.4	48.0	17	1	AR048076	ACCESSION:AR048076
	2	14.4	48.0	17	1	AR048079	ACCESSION:AR048079
	3	14.4	48.0	17	1	AR108979	ACCESSION:AR108979
	4	14.4	48.0	17	1	AR108982	ACCESSION:AR108982
	5	14.4	48.0	18	1	AR048082	ACCESSION:AR048082
	6	14.4	48.0	18	1	AR108985	ACCESSION:AR108985
	7	13.8	46.0	17	1	A20708	ACCESSION:A20708
	8	13.8	46.0	17	1	A21027	ACCESSION:A21027
	9	13.8	46.0	17	1	BD249433	ACCESSION:BD249433
	10	13.8	46.0	17	1	AR340497	ACCESSION:AR340497
	11	13.8	46.0	17	1	AX008727	ACCESSION:AX008727
	12	13.8	46.0	17	1	AX325661	ACCESSION:AX325661
c	13	13.8	46.0	17	1	AX325662	ACCESSION:AX325662
	14	13.8	46.0	18	1	A21030	ACCESSION:A21030
	15	13.8	46.0	18	1	AR048072	ACCESSION:AR048072
	16	13.8	46.0	18	1	AR108975	ACCESSION:AR108975
	17	13.8	46.0	18	1	BD249435	ACCESSION:BD249435
	18	13.8	46.0	18	1	AR340499	ACCESSION:AR340499
	19	13.8	46.0	18	1	AX008729	ACCESSION:AX008729
	20	13.8	46.0	18	1	AX084246	ACCESSION:AX084246
c	21	13.8	46.0	18	1	AX084249	ACCESSION:AX084249
	22	12.8	42.7	17	1	AR048077	ACCESSION:AR048077
	23	12.8	42.7	17	1	AR048078	ACCESSION:AR048078
	24	12.8	42.7	17	1	AR048080	ACCESSION:AR048080
	25	12.8	42.7	17	1	AR048081	ACCESSION:AR048081
	26	12.8	42.7	17	1	AR108980	ACCESSION:AR108980
	27	12.8	42.7	17	1	AR108981	ACCESSION:AR108981
	28	12.8	42.7	17	1	AR108983	ACCESSION:AR108983
	29	12.8	42.7	17	1	AR108984	ACCESSION:AR108984
c	30	12	40.0	14	1	BD209410	ACCESSION:BD209410
c	31	12	40.0	15	1	A12791	ACCESSION:A12791
c	32	11.4	38.0	15	1	I27893	ACCESSION:I27893
	33	11	36.7	14	1	A89566	ACCESSION:A89566
	34	11	36.7	14	1	A89567	ACCESSION:A89567
	35	11	36.7	14	1	BD067079	ACCESSION:BD067079
	36	11	36.7	14	1	BD067080	ACCESSION:BD067080
c	37	10.8	36.0	14	1	BD209394	ACCESSION:BD209394
	38	10	33.3	10	1	BD239909	ACCESSION:BD239909
c	39	10	33.3	12	1	A71513	ACCESSION:A71513
	40	10	33.3	13	1	AX003113	ACCESSION:AX003113
c	41	9.4	31.3	11	1	AX623670	ACCESSION:AX623670
c	42	9.4	31.3	11	1	AX629388	ACCESSION:AX629388
	43	9.4	31.3	11	1	AX629909	ACCESSION:AX629909
c	44	9.4	31.3	11	1	AX630102	ACCESSION:AX630102
c	45	9.4	31.3	11	1	AX631091	ACCESSION:AX631091
c	46	9.4	31.3	12	1	AR167701	ACCESSION:AR167701
c	47	9.4	31.3	12	1	E29585	ACCESSION:E29585
c	48	9.4	31.3	12	1	E38691	ACCESSION:E38691
c	49	9.4	31.3	12	1	E64117	ACCESSION:E64117
c	50	9.4	31.3	12	1	BD061483	ACCESSION:BD061483
c	51	9.4	31.3	12	1	BD101930	ACCESSION:BD101930
c	52	9	30.0	10	1	BD240229	ACCESSION:BD240229
	53	9	30.0	10	1	BD248497	ACCESSION:BD248497
c	54	9	30.0	10	1	AR303300	ACCESSION:AR303300
	55	9	30.0	10	1	AX510716	ACCESSION:AX510716
c	56	9	30.0	11	1	AX471386	ACCESSION:AX471386
c	57	9	30.0	11	1	AX625231	ACCESSION:AX625231
	58	9	30.0	11	1	AX626985	ACCESSION:AX626985
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c	60	9	30.0	11	1	AX630058	ACCESSION:AX630058
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	63	8.4	28.0	10	1	AR161933	ACCESSION:AR161933
	64	8.4	28.0	10	1	BD240233	ACCESSION:BD240233
c	65	8.4	28.0	10	1	E54684	ACCESSION:E54684
c	66	8.4	28.0	10	1	AR181983	ACCESSION:AR181983
	67	8.4	28.0	10	1	AR303303	ACCESSION:AR303303
c	68	8.4	28.0	10	1	AR303338	ACCESSION:AR303338
	69	8.4	28.0	10	1	AR304485	ACCESSION:AR304485
	70	8.4	28.0	10	1	AR382219	ACCESSION:AR382219
c	71	8.4	28.0	10	1	AX152226	ACCESSION:AX152226
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	76	8.4	28.0	10	1	BD065117	ACCESSION:BD065117
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	78	8.4	28.0	11	1	A02163	ACCESSION:A02163
	79	8.4	28.0	11	1	A04685	ACCESSION:A04685
c	80	8.4	28.0	11	1	AR030153	ACCESSION:AR030153
c	81	8.4	28.0	11	1	AR353840	ACCESSION:AR353840
c	82	8.4	28.0	11	1	AX470484	ACCESSION:AX470484
	83	8.4	28.0	11	1	AX470732	ACCESSION:AX470732
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c	87	8.4	28.0	11	1	AX625489	ACCESSION:AX625489
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c	89	8.4	28.0	11	1	AX626847	ACCESSION:AX626847
c	90	8.4	28.0	11	1	AX627093	ACCESSION:AX627093
	91	8.4	28.0	11	1	AX627287	ACCESSION:AX627287
	92	8.4	28.0	11	1	AX627505	ACCESSION:AX627505
c	93	8.4	28.0	11	1	AX627654	ACCESSION:AX627654
	94	8.4	28.0	11	1	AX627926	ACCESSION:AX627926
	95	8.4	28.0	11	1	AX628508	ACCESSION:AX628508
	96	8.4	28.0	11	1	AX629116	ACCESSION:AX629116
c	97	8.4	28.0	11	1	AX629158	ACCESSION:AX629158
	98	8.4	28.0	11	1	AX629366	ACCESSION:AX629366
c	99	8.4	28.0	11	1	AX629825	ACCESSION:AX629825
c	100	8.4	28.0	11	1	AX629827	ACCESSION:AX629827
	101	8.4	28.0	11	1	AX630195	ACCESSION:AX630195
c	102	8.4	28.0	11	1	AX632012	ACCESSION:AX632012

ALIGNMENTS

```
RESULT 1
AR048076
LOCUS       AR048076                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 17 from patent US 5821046.
ACCESSION   AR048076
VERSION     AR048076.1  GI:5970419
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 17 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"

  Query Match            48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 9.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 2
AR048079
LOCUS       AR048079                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5821046.
ACCESSION   AR048079
VERSION     AR048079.1  GI:5970422
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 20 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"

  Query Match            48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 9.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 3
AR108979
LOCUS       AR108979                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 17 from patent US 6114109.
ACCESSION   AR108979
VERSION     AR108979.1  GI:12825255
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 17 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 9.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 4
AR108982
LOCUS       AR108982                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 20 from patent US 6114109.
ACCESSION   AR108982
VERSION     AR108982.1  GI:12825258
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 20 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"

  Query Match            48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 9.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 5
AR048082
LOCUS       AR048082                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 23 from patent US 5821046.
ACCESSION   AR048082
VERSION     AR048082.1  GI:5970425
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 23 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="unassigned DNA"

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Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 6
AR108985
LOCUS       AR108985                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6114109.
ACCESSION   AR108985
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VERSION     AR108985.1  GI:12825261
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 23 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="unassigned DNA"

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  Best Local Similarity   88.2%;  Pred. No. 9.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGANTTGAGCAGC 17


RESULT 7
A20708
LOCUS       A20708                    17 bp    RNA     linear   PAT 03-OCT-1994
DEFINITION  Oligoribonucleotide 17-mer.
ACCESSION   A20708
VERSION     A20708.1  GI:641287
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   .
  TITLE     VIRAL (HIV) GROWTH INHIBITION
  JOURNAL   Patent: WO 9202228-A 2 20-FEB-1992;
FEATURES             Location/Qualifiers
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  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 8
A21027
LOCUS       A21027                    17 bp    RNA     linear   PAT 03-OCT-1994
DEFINITION  Oligoribonucleotide.
ACCESSION   A21027
VERSION     A21027.1  GI:641329
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   .
  TITLE     VIRAL (HIV) GROWTH INHIBITION
  JOURNAL   Patent: WO 9202228-A 17 20-FEB-1992;
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
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  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 9
BD249433
LOCUS       BD249433                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and kits for discovery of RNA-binding compounds.
ACCESSION   BD249433
VERSION     BD249433.1  GI:33059203
KEYWORDS    JP 2002526032-A/1.
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J. and Prescott,C.D.
  TITLE     Methods and kits for discovery of RNA-binding compounds
  JOURNAL   Patent: JP 2002526032-A 1 20-AUG-2002;
            RIBOTARGETS LTD
COMMENT     OS   HIV
            PN   JP 2002526032-A/1
            PD   20-AUG-2002
            PF   04-JUN-1999 JP 2000553615
            PR   05-JUN-1998 GB    9812196.5,02-MAR-1999 GB    9904790.4 PI
            JONATHAN KARN,CATHERINE DENISE PRESCOTT
            PC   C12Q1/68,C12N15/09,G01N21/78,G01N33/53,G01N33/542,G01N33/566,
            PC   G01N37/00,
            PC   C12N15/00
            CC   Methods and kits for discovery of RNA-binding compounds FH
            Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='HIV'.
FEATURES             Location/Qualifiers
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  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 10
AR340497
LOCUS       AR340497                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6573045.
ACCESSION   AR340497
VERSION     AR340497.1  GI:33732097
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J. and Prescott,C.D.
  TITLE     Methods and kits for discovery of RNA-binding compounds
  JOURNAL   Patent: US 6573045-A 1 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .17
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  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 11
AX008727
LOCUS       AX008727                  17 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 1 from Patent WO9964625.
ACCESSION   AX008727
VERSION     AX008727.1  GI:9996224
KEYWORDS    .
SOURCE      Human immunodeficiency virus
  ORGANISM  Human immunodeficiency virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
  AUTHORS   Prescott,C.D. and Karn,J.
  TITLE     Methods and kits for discovery of rna-binding compounds
  JOURNAL   Patent: WO 9964625-A 1 16-DEC-1999;
            RIBOTARGETS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Human immunodeficiency virus"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:12721"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 12
AX325661
LOCUS       AX325661                  17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 1799 from Patent WO0192512.
ACCESSION   AX325661
VERSION     AX325661.1  GI:18096420
KEYWORDS    .
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 1799 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Solanum tuberosum"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4113"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAGACTTCA 1501
              |||||||| | ||||||
Db          1 CAAGAAGCTAAACTTCA 17


RESULT 13
AX325662/c
LOCUS       AX325662                  17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 1800 from Patent WO0192512.
ACCESSION   AX325662
VERSION     AX325662.1  GI:18096421
KEYWORDS    .
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 1800 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Solanum tuberosum"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4113"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAGACTTCA 1501
              |||||||| | ||||||
Db         17 CAAGAAGCTAAACTTCA 1


RESULT 14
A21030
LOCUS       A21030                    18 bp    RNA     linear   PAT 03-OCT-1994
DEFINITION  Oligoribonucleotide 18-mer.
ACCESSION   A21030
VERSION     A21030.1  GI:641332
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     VIRAL (HIV) GROWTH INHIBITION
  JOURNAL   Patent: WO 9202228-A 20 20-FEB-1992;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 15
AR048072
LOCUS       AR048072                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5821046.
ACCESSION   AR048072
VERSION     AR048072.1  GI:5970415
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
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  JOURNAL   Patent: US 5821046-A 13 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 16
AR108975
LOCUS       AR108975                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 13 from patent US 6114109.
ACCESSION   AR108975
VERSION     AR108975.1  GI:12825251
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 13 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 17
BD249435
LOCUS       BD249435                 18 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and kits for discovery of RNA-binding compounds.
ACCESSION   BD249435
VERSION     BD249435.1  GI:33059205
KEYWORDS    JP 2002526032-A/3.
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J. and Prescott,C.D.
  TITLE     Methods and kits for discovery of RNA-binding compounds
  JOURNAL   Patent: JP 2002526032-A 3 20-AUG-2002;
            RIBOTARGETS LTD
COMMENT     OS   HIV
            PN   JP 2002526032-A/3
            PD   20-AUG-2002
            PF   04-JUN-1999 JP 2000553615
            PR   05-JUN-1998 GB    9812196.5,02-MAR-1999 GB    9904790.4 PI
            JONATHAN KARN,CATHERINE DENISE PRESCOTT
            PC   C12Q1/68,C12N15/09,G01N21/78,G01N33/53,G01N33/542,G01N33/566,
            PC   G01N37/00,
            PC   C12N15/00
            CC   Methods and kits for discovery of RNA-binding compounds FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='HIV'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Human immunodeficiency virus 1"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:11676"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 18
AR340499
LOCUS       AR340499                 18 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6573045.
ACCESSION   AR340499
VERSION     AR340499.1  GI:33732099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Karn,J. and Prescott,C.D.
  TITLE     Methods and kits for discovery of RNA-binding compounds
  JOURNAL   Patent: US 6573045-A 3 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17


RESULT 19
AX008729
LOCUS       AX008729                 18 bp    RNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 3 from Patent WO9964625.
ACCESSION   AX008729
VERSION     AX008729.1  GI:9996226
KEYWORDS    .
SOURCE      Human immunodeficiency virus
  ORGANISM  Human immunodeficiency virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
  AUTHORS   Prescott,C.D. and Karn,J.
  TITLE     Methods and kits for discovery of rna-binding compounds
  JOURNAL   Patent: WO 9964625-A 3 16-DEC-1999;
            RIBOTARGETS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Human immunodeficiency virus"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:12721"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| || ||||||
Db          1 AGCCAGATTTGAGCAGC 17
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RESULT 20
AX084246
LOCUS       AX084246                 18 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 40 from Patent WO0110902.
ACCESSION   AX084246
VERSION     AX084246.1  GI:13185749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Fernandes,E.
  TITLE     Nucleic acids and secreted polypeptides encoded thereby
  JOURNAL   Patent: WO 0110902-A 40 15-FEB-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR PRIMER"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
              | ||||||||||||| |
Db          2 CTACCAAGAAGCCAGCC 18


RESULT 21
AX084249/c
LOCUS       AX084249                 18 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 43 from Patent WO0110902.
ACCESSION   AX084249
VERSION     AX084249.1  GI:13185752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Fernandes,E.
  TITLE     Nucleic acids and secreted polypeptides encoded thereby
  JOURNAL   Patent: WO 0110902-A 43 15-FEB-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR PRIMER"

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
              | ||||||||||||| |
Db         17 CTACCAAGAAGCCAGCC 1


RESULT 22
AR048077
LOCUS       AR048077                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 18 from patent US 5821046.
ACCESSION   AR048077
VERSION     AR048077.1  GI:5970420
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 18 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| | ||||||
Db          1 AGCCAGATNTGAGCAGC 17


RESULT 23
AR048078
LOCUS       AR048078                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 19 from patent US 5821046.
ACCESSION   AR048078
VERSION     AR048078.1  GI:5970421
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 19 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| |  ||||||
Db          1 AGCCAGATTNGAGCAGC 17


RESULT 24
AR048080
LOCUS       AR048080                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 21 from patent US 5821046.
ACCESSION   AR048080
VERSION     AR048080.1  GI:5970423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 21 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| | ||||||
Db          1 AGCCAGATNTCAGCAGC 17
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RESULT 25
AR048081
LOCUS       AR048081                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5821046.
ACCESSION   AR048081
VERSION     AR048081.1  GI:5970424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
  TITLE     RNA oligonucleotides that bind HIV tat protein
  JOURNAL   Patent: US 5821046-A 22 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| |  ||||||
Db          1 AGCCAGATTNGAGCAGC 17


RESULT 26
AR108980
LOCUS       AR108980                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 18 from patent US 6114109.
ACCESSION   AR108980
VERSION     AR108980.1  GI:12825256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 18 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              |||||||  | ||||||
Db          1 AGCCAGATNTGAGCAGC 17


RESULT 27
AR108981
LOCUS       AR108981                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 19 from patent US 6114109.
ACCESSION   AR108981
VERSION     AR108981.1  GI:12825257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 19 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| |  ||||||
Db          1 AGCCAGATTNGAGCAGC 17


RESULT 28
AR108983
LOCUS       AR108983                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 21 from patent US 6114109.
ACCESSION   AR108983
VERSION     AR108983.1  GI:12825259
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 21 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              |||||||  | ||||||
Db          1 AGCCAGATNTGAGCAGC 17


RESULT 29
AR108984
LOCUS       AR108984                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 22 from patent US 6114109.
ACCESSION   AR108984
VERSION     AR108984.1  GI:12825260
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Karn,J., Gait,M.J., Heaphy,S. and Dingwall,C.
  TITLE     Viral (HIV) growth inhibition
  JOURNAL   Patent: US 6114109-A 22 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 16;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| |  ||||||
Db          1 AGCCAGATTNGAGCAGC 17


RESULT 30
BD209410/c
LOCUS       BD209410                  14 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209410
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VERSION     BD209410.1  GI:33019180
KEYWORDS    JP 2002512791-A/3000.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 3000 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/3000
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                 virus)'.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="unidentified"
                    /mol_type="genomic RNA"
                    /db_xref="taxon:32644"

  Query Match             40.0%;  Score 12;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGCCA 1508
              ||||||||||||
Db         12 CTTCAGCAGCCA 1


RESULT 31
A12791/c
LOCUS       A12791                    15 bp    DNA     linear   PAT 28-APR-1994
DEFINITION  oligonucleotide from clone pHD 119.
ACCESSION   A12791
VERSION     A12791.1  GI:512655
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   .
  TITLE     A DNA SEQUENCE
  JOURNAL   Patent: WO 8605804-A 22 09-OCT-1986;
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"

  Query Match             40.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGCCA 1508
              ||||||||||||
Db         15 CTTCAGCAGCCA 4


RESULT 32
I27893/c
LOCUS       I27893                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 65 from patent US 5567809.
ACCESSION   I27893
VERSION     I27893.1  GI:1818669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
  TITLE     Methods and reagents for HLA DRbeta DNA typing
  JOURNAL   Patent: US 5567809-A 65 22-OCT-1996;
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             38.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 24;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1494 AGACTTCAGCAGC 1506
              |||||| ||||||
Db         15 AGACTTAAGCAGC 3


RESULT 33
A89566
LOCUS       A89566                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1714 from Patent WO9833904.
ACCESSION   A89566
VERSION     A89566.1  GI:6738136
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1714 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"

  Query Match             36.7%;  Score 11;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCCA 1508
              ||||||||||||
Db          2 TTCAGCAGCCA 12


RESULT 34
A89567
LOCUS       A89567                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1715 from Patent WO9833904.
ACCESSION   A89567
VERSION     A89567.1  GI:6738137
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1715 06-AUG-1998;
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          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             36.7%;  Score 11;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCCA 1508
              ||||||||||
Db          4 TTCAGCAGCCA 14


RESULT 35
BD067079
LOCUS       BD067079                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD067079
VERSION     BD067079.1  GI:22612682
KEYWORDS    JP 2001511000-A/1714.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 1714 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/1714
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             36.7%;  Score 11;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCCA 1508
              ||||||||||
Db          2 TTCAGCAGCCA 12


RESULT 36
BD067080
LOCUS       BD067080                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD067080
VERSION     BD067080.1  GI:22612683
KEYWORDS    JP 2001511000-A/1715.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 1715 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/1715
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             36.7%;  Score 11;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCCA 1508
              ||||||||||
Db          4 TTCAGCAGCCA 14


RESULT 37
BD209394/c
LOCUS       BD209394                  14 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209394
VERSION     BD209394.1  GI:33019164
KEYWORDS    JP 2002512791-A/2984.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 2984 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/2984
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             36.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 28;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAGCCA 1508
              || || ||||||||
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Db         14 GAGTTGAGCAGCCA 1


RESULT 38
BD239909
LOCUS       BD239909                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239909
VERSION     BD239909.1  GI:33049679
KEYWORDS    JP 2002534056-A/1327.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1327 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1327
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
             ||||||||||
Db          1 AGAAGCCAGA 10


RESULT 39
A71513/c
LOCUS       A71513                    12 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 72 from Patent WO9813521.
ACCESSION   A71513
VERSION     A71513.1  GI:4775125
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Fesce,R. and Consalez,G.
  TITLE     METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
            PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
  JOURNAL   Patent: WO 9813521-A 72 02-APR-1998;
            FESCE RICCARDO (IT)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"

  Query Match             33.3%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAG 1488
             ||||||||||
Db         10 CACGACCAAG 1


RESULT 40
AX003113
LOCUS       AX003113                  13 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 15 from Patent WO9934217.
ACCESSION   AX003113
VERSION     AX003113.1  GI:9926975
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Xu,D. and Liew,F.Y.
  TITLE     Reagents specific for st2l and uses therefor
  JOURNAL   Patent: WO 9934217-A 15 08-JUL-1999;
            XU DAMO (GB); LIEW FOO YEW (GB)
FEATURES              Location/Qualifiers
     source           1. .13
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="PRIMER"

  Query Match             33.3%;  Score 10;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
             ||||||||||
Db          4 CTTCAGCAGC 13


RESULT 41
AX623670/c
LOCUS       AX623670                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 711 from Patent WO02053774.
ACCESSION   AX623670
VERSION     AX623670.1  GI:28451611
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 711 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
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  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 39;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAG 1505
              |||| ||||||
Db         11 GACTACAGCAG 1


RESULT 42
AX629388/c
LOCUS       AX629388                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6429 from Patent WO02053774.
ACCESSION   AX629388
VERSION     AX629388.1  GI:28457426
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6429 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 39;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTT 1499
              ||||||| |||
Db         11 AAGCCAGTCTT 1


RESULT 43
AX629909
LOCUS       AX629909                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6950 from Patent WO02053774.
ACCESSION   AX629909
VERSION     AX629909.1  GI:28457947
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6950 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 39;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAGA 1496
              ||||||| |||
Db          1 AAGAAGCAAGA 11


RESULT 44
AX630102/c
LOCUS       AX630102                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7143 from Patent WO02053774.
ACCESSION   AX630102
VERSION     AX630102.1  GI:28458140
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7143 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 39;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAG 1495
              ||||||| |||
Db         11 CAAGAAGGCAG 1


RESULT 45
AX631091/c
LOCUS       AX631091                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8132 from Patent WO02053774.
ACCESSION   AX631091
VERSION     AX631091.1  GI:28459135
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8132 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 39;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAG 1505
              |||| ||||||
Db         11 GACTACAGCAG 1


RESULT 46
AR167701/c
LOCUS       AR167701                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 65 from patent US 6287769.
ACCESSION   AR167701
VERSION     AR167701.1  GI:17903498
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
```

```
  TITLE     Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
  JOURNAL   Patent: US 6287769-A 65 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 47
E29585/c
LOCUS       E29585                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste.
ACCESSION   E29585
VERSION     E29585.1  GI:13021088
KEYWORDS    JP 1999276176-A/65.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
  JOURNAL   Patent: JP 1999276176-A 65 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 1999276176-A/65
            PD   12-OCT-1999
            PF   31-MAR-1998 JP 1998087652
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 48
E38691/c
LOCUS       E38691                    12 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and device for amplifying DNA fragment.
ACCESSION   E38691
VERSION     E38691.1  GI:18621353
KEYWORDS    JP 2000270867-A/65.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,K.
  TITLE     Method and device for amplifying DNA fragment
  JOURNAL   Patent: JP 2000270867-A 65 03-OCT-2000;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 2000270867-A/65
            PD   03-OCT-2000
            PF   19-MAR-1999 JP 1999076844
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 49
E64117/c
LOCUS       E64117                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, amplification apparatus of DNA
             fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating  substance.
ACCESSION   E64117
VERSION     E64117.1  GI:13019521
KEYWORDS    JP 1999341989-A/65.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
  JOURNAL   Patent: JP 1999341989-A 65 14-DEC-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 1999341989-A/65
            PD   14-DEC-1999
            PF   16-MAR-1999 JP 1999069694
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
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  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
              ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 50
BD061483/c
LOCUS       BD061483                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for discriminating microorganisms, apparatus for
            discriminating microorganisms, method for preparing data base for
            discriminating microorganisms, and recording medium recorded with
            program for discriminating microorganisms.
ACCESSION   BD061483
VERSION     BD061483.1  GI:22607089
KEYWORDS    JP 2001275700-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,K.
  TITLE     Method for discriminating microorganisms, apparatus for
            discriminating microorganisms, method for preparing data base for
            discriminating microorganisms, and recording medium recorded with
            program for discriminating microorganisms
  JOURNAL   Patent: JP 2001275700-A 10 09-OCT-2001;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 2001275700-A/10
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000099482
            PI   KOICHI INOUE
            PC   C12Q1/68,C12M1/00,C12M1/34,C12N15/09,G06F17/30,C12N15/00 CC
            Primer
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .12
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
              ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 51
BD101930/c
LOCUS       BD101930                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method of discriminating microorganisms, apparatus for
            discriminating microorganisms, method of making database for
            discriminating microorganisms, microorganisms discriminating
            program and record medium for recording the same.
ACCESSION   BD101930
VERSION     BD101930.1  GI:22647504
KEYWORDS    WO 0175156-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
  TITLE     Method of discriminating microorganisms, apparatus for
            discriminating microorganisms, method of making database for
            discriminating microorganisms, microorganisms discriminating
            program and record medium for recording the same
  JOURNAL   Patent: WO 0175156-A 10 11-OCT-2001;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES, TAKAKAZU INOUE
COMMENT     OS   Artificial Sequence
            PN   WO 0175156-A/10
            PD   11-OCT-2001
            PF   27-MAR-2001 WO 2001JP002516
            PR   31-MAR-2000 JP 00P   099482
            PI   TAKAKAZU INOUE
            PC   C12Q1/68,C12N15/10,G01N33/48,G01N27/447,G06F17/30,C12M1/00 CC
             Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .12
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 41;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
              ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 52
BD240229/c
LOCUS       BD240229                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240229
VERSION     BD240229.1  GI:33049999
KEYWORDS    JP 2002534056-A/1647.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1647 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1647
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES                Location/Qualifiers
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    source          1. .10
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 53
BD248497
LOCUS       BD248497                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  T cells specific for target antigens and methods and vaccines based
            thereon.
ACCESSION   BD248497
VERSION     BD248497.1  GI:33058267
KEYWORDS    JP 2002529082-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zauderer,M.
  TITLE     T cells specific for target antigens and methods and vaccines based
            thereon
  JOURNAL   Patent: JP 2002529082-A 11 10-SEP-2002;
            UNIVERSITY OF ROCHESTER
COMMENT     OS   Artificial Sequence
            PN   JP 2002529082-A/11
            PD   10-SEP-2002
            PF   10-NOV-1998 JP 2000581183
            PI   MAURICE ZAUDERER
            PC   C12N15/09,A01K67/027,A61K35/76,A61K39/00,A61K39/04,A61K39/12,
            PC   A61K39/395,
            PC   A61K39/395,A61P31/04,A61P31/10,A61P31/12,A61P35/00,C12N5/10,
            PC   C12Q1/02,
            PC   G01N33/574,C12N15/00,C12N5/00
            CC   MR7
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
              |||||||||
Db          2 CAGACTTCA 10


RESULT 54
AR303300/c
LOCUS       AR303300                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 25 from patent US 6544736.
ACCESSION   AR303300
VERSION     AR303300.1  GI:31692076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 25 08-APR-2003;
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unknown"
                    /mol_type="genomic DNA"

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAG 1505
              |||||||||
Db         10 CTTCAGCAG 2


RESULT 55
AX510716
LOCUS       AX510716                  10 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4 from Patent WO0227027.
ACCESSION   AX510716
VERSION     AX510716.1  GI:23391953
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Zauderer,M.
  TITLE     Method of screening for therapeutics for infectious diseases
  JOURNAL   Patent: WO 0227027-A 4 04-APR-2002;
            THE UNIVERSITY OF ROCHESTER (US)
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Oligonucleotide primer"

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
              |||||||||
Db          2 CAGACTTCA 10


RESULT 56
AX471386/c
LOCUS       AX471386                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 963 from Patent WO02053773.
ACCESSION   AX471386
VERSION     AX471386.1  GI:22206511
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 963 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES            Location/Qualifiers
     source         1. .11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1490 AGCCAGACT 1498
              |||||||||
Db         11 AGCCAGACT 3


RESULT 57
AX625231/c
LOCUS       AX625231                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2272 from Patent WO02053774.
ACCESSION   AX625231
VERSION     AX625231.1  GI:28453172
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2272 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACT 1498
              |||||||||
Db         11 AGCCAGACT 3


RESULT 58
AX626985
LOCUS       AX626985                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4026 from Patent WO02053774.
ACCESSION   AX626985
VERSION     AX626985.1  GI:28455023
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4026 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGC 1506
              |||||||||
Db          1 TTCAGCAGC 9


RESULT 59
AX628452/c
LOCUS       AX628452                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5493 from Patent WO02053774.
ACCESSION   AX628452
VERSION     AX628452.1  GI:28456490
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5493 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         11 CAGCAGCCA 3


RESULT 60
AX630058/c
LOCUS       AX630058                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7099 from Patent WO02053774.
ACCESSION   AX630058
VERSION     AX630058.1  GI:28458096
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7099 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 61
AX632652/c
LOCUS       AX632652                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9694 from Patent WO02053774.
ACCESSION   AX632652
VERSION     AX632652.1  GI:28468267
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9694 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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    source          1. .11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACT 1498
              |||||||||
Db         11 AGCCAGACT 3


RESULT 62
AR070986
LOCUS       AR070986                  10 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 20 from patent US 5908978.
ACCESSION   AR070986
VERSION     AR070986.1  GI:7221874
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Amerson,H.V., Wilcox,P., Sederoff,R.R., Kuhlman,E.George.,
            O'Malley,D.M. and Grattapaglia,D.
  TITLE     Methods for within family selection of disease resistance in woody
            perennials using genetic markers
  JOURNAL   Patent: US 5908978-A 20 01-JUN-1999;
FEATURES             Location/Qualifiers
    source           1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              |||||||| |
Db          1 GAAGCCAGCC 10


RESULT 63
AR161933
LOCUS       AR161933                  10 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6258537.
ACCESSION   AR161933
VERSION     AR161933.1  GI:16228965
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Keinath,A.P., Somai,B.M. and Dean,R.A.
  TITLE     Method of diagnosing gummy stem blight in plants using a polymerase
            chain reaction assay
  JOURNAL   Patent: US 6258537-A 6 10-JUL-2001;
FEATURES             Location/Qualifiers
    source           1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              || |||||||
Db          1 GATGCCAGAC 10


RESULT 64
BD240233
LOCUS       BD240233                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240233
VERSION     BD240233.1  GI:33050003
KEYWORDS    JP 2002534056-A/1651.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1651 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1651
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
    source           1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              |||||||| |
Db          1 GAAGCCAGCC 10


RESULT 65
E54684/c
LOCUS       E54684                    10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54684
VERSION     E54684.1  GI:22556167
KEYWORDS    JP 2001211883-A/36.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
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  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 36 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/36
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              | ||||||||
Db         10 AGGCCAGACT 1


RESULT 66
AR181983/c
LOCUS       AR181983                  10 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 12 from patent US 6337071.
ACCESSION   AR181983
VERSION     AR181983.1  GI:20224899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Molyneux,W.Mitchell.
  TITLE     Mosquito and/or flea control
  JOURNAL   Patent: US 6337071-A 12 08-JAN-2002;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              ||| ||||||
Db         10 TTCTGCAGCC 1


RESULT 67
AR303303
LOCUS       AR303303                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 28 from patent US 6544736.
ACCESSION   AR303303
VERSION     AR303303.1  GI:31692079
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 28 08-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCAG 1505
              || |||||||
Db          1 ACATCAGCAG 10


RESULT 68
AR303338/c
LOCUS       AR303338                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 63 from patent US 6544736.
ACCESSION   AR303338
VERSION     AR303338.1  GI:31692114
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 63 08-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCA 1504
              ||||||| ||
Db         10 GACTTCACCA 1


RESULT 69
AR304485
LOCUS       AR304485                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 110 from patent US 6544784.
ACCESSION   AR304485
VERSION     AR304485.1  GI:31693633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Bullerdiek,J., Van de Ven,W.J.M., Schoenmakers,H.F.P.M. and Mols,R.
  TITLE     Multiple-tumor aberrant growth genes
  JOURNAL   Patent: US 6544784-A 110 08-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||||| |||
Db          1 AAGAAGGCAG 10


RESULT 70
AR382219
LOCUS       AR382219                  10 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6610487.
ACCESSION   AR382219
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VERSION     AR382219.1  GI:40090631
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Keinath,A.P., Somai,B.M. and Dean,R.A.
  TITLE     Method of diagnosing gummy stem blight in plants using a polymerase
            chain reaction assay
  JOURNAL   Patent: US 6610487-A 6 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              || |||||||
Db          1 GATGCCAGAC 10


RESULT 71
AX152226/c
LOCUS       AX152226                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 141 from Patent WO0138577.
ACCESSION   AX152226
VERSION     AX152226.1  GI:14533877
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 141 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCAG 1505
              |||| |||||
Db         10 ACTTAAGCAG 1


RESULT 72
AX152377
LOCUS       AX152377                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 292 from Patent WO0138577.
ACCESSION   AX152377
VERSION     AX152377.1  GI:14534028
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 292 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1499 TCAGCAGCCA 1508
              ||| ||||||
Db          1 TCAACAGCCA 10


RESULT 73
AX153162/c
LOCUS       AX153162                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1077 from Patent WO0138577.
ACCESSION   AX153162
VERSION     AX153162.1  GI:14534813
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1077 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTT 1499
              |||||| |||
Db         10 AGCCAGTCTT 1


RESULT 74
AX362608
LOCUS       AX362608                 10 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 42 from Patent WO0208425.
ACCESSION   AX362608
VERSION     AX362608.1  GI:18694752
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Finkel,K. and Koshy,B.
  TITLE     Haplotypes of the adrb3 gene
  JOURNAL   Patent: WO 0208425-A 42 31-JAN-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              ||| ||||||
Db          1 CCAGGAAGCC 10
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RESULT 75
AX377325/c
LOCUS       AX377325                 10 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 63 from Patent WO0212498.
ACCESSION   AX377325
VERSION     AX377325.1  GI:19573612
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kliem,S.E., Koshy,B. and Tanguay,D.A.
  TITLE     Haplotypes of the isl1 gene
  JOURNAL   Patent: WO 0212498-A 63 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCA 1504
              | ||||||||
Db         10 GGCTTCAGCA 1


RESULT 76
BD065117
LOCUS       BD065117                 10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065117
VERSION     BD065117.1  GI:22610720
KEYWORDS    JP 2001509017-A/53.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 53 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/53
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Saccharomyces cerevisiae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4932"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGA 1489
              ||| ||||||
Db          1 ACGGCCAAGA 10


RESULT 77
BD167088/c
LOCUS       BD167088                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167088
VERSION     BD167088.1  GI:27872900
KEYWORDS    JP 2002209591-A/633.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 633 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/633
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              | ||||||||
Db         10 AGGCCAGACT 1


RESULT 78
A02163
LOCUS       A02163                   11 bp    DNA     linear   PAT 21-MAY-1993
DEFINITION  Nucleotide sequence 10 from patent number WO8503723.
ACCESSION   A02163
VERSION     A02163.1  GI:410850
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   .
  TITLE     VECTOR FOR THE EXPRESSION IN YEASTS OF INTERLEUKINE-2, TRANSFORMED
            YEASTS AND METHOD FOR PREPARING INTERLEUKINE-2
  JOURNAL   Patent: WO 8503723-A 10 29-AUG-1985;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAA 1490
              |||| |||||
Db          1 CGACAAAGAA 10
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RESULT 79
A04685
LOCUS       A04685                    11 bp    DNA     linear   PAT 24-MAY-1993
DEFINITION  Nucleotide sequence 9 from patent number EP0152358.
ACCESSION   A04685
VERSION     A04685.1  GI:411035
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Lemoine,Y., Sondermeyer,P., Loison,G., Aigle,M. and Lecocq,J.P.
  TITLE     Yeast-expression vectors for interleukin-2, transformed yeasts and
            process for the preparation of interleukin-2
  JOURNAL   Patent: EP 0152358-A 9 21-AUG-1985;
            TRANSGENE S.A
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAA 1490
              |||| |||||
Db          1 CGACAAAGAA 10


RESULT 80
AR030153/c
LOCUS       AR030153                  11 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 342 from patent US 5861244.
ACCESSION   AR030153
VERSION     AR030153.1  GI:5943367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 342 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1482 GACCAAGAAG 1491
              || |||||||
Db         11 GAACAAGAAG 2


RESULT 81
AR353840/c
LOCUS       AR353840                  11 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6593111.
ACCESSION   AR353840
VERSION     AR353840.1  GI:33759907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Baric,R.S. and Yount,B.
  TITLE     Directional assembly of large viral genomes and chromosomes
  JOURNAL   Patent: US 6593111-A 15 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              |||||||| |
Db         10 CCAAGAAGGC 1


RESULT 82
AX470484/c
LOCUS       AX470484                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 61 from Patent WO02053773.
ACCESSION   AX470484
VERSION     AX470484.1  GI:22205609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 61 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              |||| |||||
Db         11 TTCACCAGCC 2


RESULT 83
AX470732
LOCUS       AX470732                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 309 from Patent WO02053773.
ACCESSION   AX470732
VERSION     AX470732.1  GI:22205857
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 309 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       1484 CCAAGAAGCC 1493
              |||||| |||
Db          2 CCAAGATGCC 11


RESULT 84
AX471384/c
LOCUS       AX471384                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 961 from Patent WO02053773.
ACCESSION   AX471384
VERSION     AX471384.1  GI:22206509
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 961 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAG 1488
              |||||||| |
Db         11 CACGACCACG 2


RESULT 85
AX616455/c
LOCUS       AX616455                  11 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 16 from Patent EP1262565.
ACCESSION   AX616455
VERSION     AX616455.1  GI:28447498
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Affourtit,J.P., Nelson,D.L., Seymour,A.B. and Webb,S.M.
  TITLE     Genetic polymorphisms in the human neurokinin 1 receptor gene and
            their uses in diagnosis and treatment of diseases
  JOURNAL   Patent: EP 1262565-A 16 04-DEC-2002;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              |||||| |||
Db         10 AAGCCATACT 1


RESULT 86
AX624591/c
LOCUS       AX624591                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1632 from Patent WO02053774.
ACCESSION   AX624591
VERSION     AX624591.1  GI:28452532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1632 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              |||| |||||
Db         11 CTTCCGCAGC 2


RESULT 87
AX625489/c
LOCUS       AX625489                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2530 from Patent WO02053774.
ACCESSION   AX625489
VERSION     AX625489.1  GI:28453430
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2530 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCAG 1502
              ||| ||||||
Db         10 CAGCCTTCAG 1


RESULT 88
AX625964
LOCUS       AX625964                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3005 from Patent WO02053774.
ACCESSION   AX625964
VERSION     AX625964.1  GI:28454002
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3005 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              |||||| |||
Db          1 AGAAGCAAGA 10


RESULT 89
AX626847/c
LOCUS       AX626847                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3888 from Patent WO02053774.
ACCESSION   AX626847
VERSION     AX626847.1  GI:28454885
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3888 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1494 AGACTTCAGC 1503
              ||||| ||||
Db         11 AGACTGCAGC 2


RESULT 90
AX627093/c
LOCUS       AX627093                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4134 from Patent WO02053774.
ACCESSION   AX627093
VERSION     AX627093.1  GI:28455131
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4134 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCAG 1502
              ||| ||||||
Db         11 CAGGCTTCAG 2


RESULT 91
AX627287
LOCUS       AX627287                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4328 from Patent WO02053774.
ACCESSION   AX627287
VERSION     AX627287.1  GI:28455325
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4328 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTT 1499
              | ||||||||
Db          2 ACCCAGACTT 11


RESULT 92
AX627505
LOCUS       AX627505                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4546 from Patent WO02053774.
ACCESSION   AX627505
VERSION     AX627505.1  GI:28455543
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4546 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              ||||||| ||
Db          1 AAGCCAGTCT 10


RESULT 93
AX627654/c
LOCUS       AX627654                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4695 from Patent WO02053774.
ACCESSION   AX627654
VERSION     AX627654.1  GI:28455692
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4695 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAG 1488
              |||||||| |
Db         11 CACGACCACG 2


RESULT 94
AX627926
LOCUS       AX627926                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4967 from Patent WO02053774.
ACCESSION   AX627926
VERSION     AX627926.1  GI:28455964
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4967 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              |||||| |||
Db          2 CTTCAGTAGC 11


RESULT 95
AX628508
LOCUS       AX628508                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5549 from Patent WO02053774.
ACCESSION   AX628508
VERSION     AX628508.1  GI:28456546
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5549 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              |||| |||||
Db          2 AGAAACCAGA 11


RESULT 96
AX629116
LOCUS       AX629116                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6157 from Patent WO02053774.
ACCESSION   AX629116
VERSION     AX629116.1  GI:28457154
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6157 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              |||||| |||
Db          2 CCAAGATGCC 11


RESULT 97
AX629158/c
LOCUS       AX629158                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6199 from Patent WO02053774.
ACCESSION   AX629158
VERSION     AX629158.1  GI:28457196
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6199 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              |||| |||||
Db         11 TTCACCAGCC 2
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RESULT 98
AX629366
LOCUS       AX629366                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6407 from Patent WO02053774.
ACCESSION   AX629366
VERSION     AX629366.1  GI:28457404
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6407 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              || |||||||
Db          2 CTCCAGCAGC 11


RESULT 99
AX629825/c
LOCUS       AX629825                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6866 from Patent WO02053774.
ACCESSION   AX629825
VERSION     AX629825.1  GI:28457863
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6866 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              ||| ||||||
Db         10 CCAGGAAGCC 1


RESULT 100
AX629827/c
LOCUS       AX629827                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6868 from Patent WO02053774.
ACCESSION   AX629827
VERSION     AX629827.1  GI:28457865
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6868 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1492 CCAGACTTCA 1501
              |||||| |||
Db         10 CCAGACATCA 1


RESULT 101
AX630195
LOCUS       AX630195                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7236 from Patent WO02053774.
ACCESSION   AX630195
VERSION     AX630195.1  GI:28458233
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7236 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              ||| ||||||
Db          2 CCAGGAAGCC 11


RESULT 102
AX632012/c
LOCUS       AX632012                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9054 from Patent WO02053774.
ACCESSION   AX632012
VERSION     AX632012.1  GI:28467627
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9054 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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/db_xref="taxon:9606"

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1497 CTTCAGCAGC 1506
              |||| |||||
Db         11 CTTCCGCAGC 2
```

Search completed: April 15, 2004, 16:33:23
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:35:35 ; Search time 0.001 Seconds
(without alignments)
98.460 Million cell updates/sec

Title: us-09-954-556-3
Perfect score: 30
Sequence: 1 cacgaccaagaagccagacttcagcagcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 143 seqs, 1641 residues

Total number of hits satisfying chosen parameters: 286

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 143 summaries

Database : rng.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13.8	46.0	17	1	AAQ24060	Artificial HIV-1 T
2	13.8	46.0	17	1	AAZ59070	HIV-1 TAR oligonuc
3	13.8	46.0	17	1	ABK26439	Waxy starch produc
c 4	13.8	46.0	17	1	ABK26440	Waxy starch produc
5	13.8	46.0	18	1	AAZ59072	HIV-1 TAR oligonuc
6	13.8	46.0	18	1	AAF74454	Human PRO2 gene-sp
c 7	13.8	46.0	18	1	AAF74457	Human PRO2 gene-sp
8	12.4	41.3	15	1	AAX57566	Antisense oligo #5
c 9	12.4	41.3	15	1	AAF49086	IGF-I oligonucleot
c 10	12.4	41.3	15	1	AAF49087	IGF-I oligonucleot
c 11	12	40.0	14	1	AAZ64832	Substrate for hair
c 12	12	40.0	14	1	ABX01669	Hepatitis C virus
c 13	12	40.0	15	1	AAF49084	IGF-I oligonucleot
c 14	12	40.0	15	1	AAF49085	IGF-I oligonucleot
c 15	11.8	39.3	15	1	AAT49619	Human CETP HH ribo
16	11.8	39.3	15	1	AAF47839	IGFBP3 oligonucleo
17	11.4	38.0	15	1	AAX57564	Antisense oligo #3
18	11.4	38.0	15	1	AAZ35973	Histoplasma capsul
c 19	11.4	38.0	15	1	AAF49088	IGF-I oligonucleot
c 20	10.8	36.0	14	1	AAZ64816	Substrate for hair
c 21	10.8	36.0	14	1	AAA99958	Geminivirus Rep re
c 22	10.8	36.0	14	1	ABX01653	Hepatitis C virus
c 23	10.4	34.7	13	1	ABF18234	Oligonucleotide SE
24	10.4	34.7	13	1	ABF18235	Oligonucleotide SE
25	10	33.3	10	1	AAZ78899	Human dendritic ce
c 26	10	33.3	10	1	AAZ83653	Metastatic breast
27	10	33.3	10	1	AAF39527	Yeast NORF gene SA
28	10	33.3	10	1	AAF34162	Yeast NORF gene SA
29	10	33.3	10	1	AAF39463	Yeast NORF gene SA
30	10	33.3	10	1	AAF41899	Yeast NORF gene SA
c 31	10	33.3	12	1	AAV32260	Random primed reve
32	10	33.3	13	1	AAX89228	PCR primer H-AP34.
33	10	33.3	13	1	ADC64953	Camellia sinensis
c 34	9.8	32.7	13	1	ABH65692	Oligonucleotide SE
c 35	9.8	32.7	13	1	ABH65694	Oligonucleotide SE
36	9.8	32.7	13	1	ABH65693	Oligonucleotide SE
37	9.8	32.7	13	1	ABH65695	Oligonucleotide SE
c 38	9.8	32.7	13	1	ABQ83680	DNA-templated synt
c 39	9.4	31.3	11	1	ABV70346	Human skin EST 813
c 40	9.4	31.3	11	1	ABV69357	Human skin EST 714
c 41	9.4	31.3	11	1	ABV62925	Human skin EST 711
c 42	9.4	31.3	11	1	ABV68643	Human skin EST 642
43	9.4	31.3	11	1	ABV69164	Human skin EST 695
c 44	9.4	31.3	12	1	AAZ41704	Organic material d
c 45	9.4	31.3	12	1	AAZ41488	Microbe detection
c 46	9.4	31.3	12	1	AAC97839	Primer used to ill
c 47	9.4	31.3	12	1	ABI02085	Oligonucleotide pr
48	9.4	31.3	12	1	ABH84038	Oligonucleotide pr
c 49	9.4	31.3	12	1	ABI53669	Oligonucleotide pr
c 50	9.4	31.3	12	1	AAI99727	Microbial SSC-PCR
c 51	9	30.0	10	1	AAX18642	p53 serial analysi
c 52	9	30.0	10	1	AAZ79219	Human dendritic ce
c 53	9	30.0	10	1	AAZ83241	Metastatic breast
c 54	9	30.0	10	1	AAZ83053	Metastatic breast
55	9	30.0	10	1	AAZ86659	Metastatic breast
56	9	30.0	10	1	AAA15242	Primer MR7 for mod
c 57	9	30.0	10	1	AAF70127	Human TNFRSF11B ge
c 58	9	30.0	10	1	AAF35009	Yeast NORF gene SA
c 59	9	30.0	10	1	AAF39472	Yeast NORF gene SA
60	9	30.0	10	1	AAF38820	Yeast NORF gene SA
61	9	30.0	10	1	AAF41980	Yeast NORF gene SA
62	9	30.0	10	1	AAF38821	Yeast NORF gene SA
63	9	30.0	10	1	AAF39528	Yeast NORF gene SA
64	9	30.0	10	1	AAF38557	Yeast NORF gene SA
65	9	30.0	10	1	AAD31785	MR 7 arbitrary pri
c 66	9	30.0	11	1	ABQ87208	Human skin stress/
c 67	9	30.0	11	1	ABV69313	Human skin EST 709
c 68	9	30.0	11	1	ABV71907	Human skin EST 969
c 69	9	30.0	11	1	ABV64486	Human skin EST 227
70	9	30.0	11	1	ABV66240	Human skin EST 402
c 71	9	30.0	11	1	ABV67707	Human skin EST 549
c 72	9	30.0	12	1	AAQ57385	Enzymatic RNA mole
73	9	30.0	12	1	ABI55792	Oligonucleotide pr
74	9	30.0	12	1	ABH93993	Oligonucleotide pr
c 75	9	30.0	12	1	ABH84166	Oligonucleotide pr
c 76	9	30.0	12	1	ABI32013	Oligonucleotide pr
77	9	30.0	12	1	ABI77576	Oligonucleotide pr
78	8.4	28.0	10	1	AAQ99836	Eucalyptus wood vo
79	8.4	28.0	10	1	AAV50097	Yeast tag for puta
80	8.4	28.0	10	1	AAX59809	Primer V7 for ampl
81	8.4	28.0	10	1	AAZ22666	T18 primer for amp
82	8.4	28.0	10	1	AAZ79223	Human dendritic ce
83	8.4	28.0	10	1	AAZ82715	Metastatic breast
c 84	8.4	28.0	10	1	AAZ81205	Metastatic breast
85	8.4	28.0	10	1	AAZ82619	Metastatic breast
86	8.4	28.0	10	1	AAZ84503	Metastatic breast
87	8.4	28.0	10	1	AAZ84255	Metastatic breast
c 88	8.4	28.0	10	1	AAZ81942	Metastatic breast
89	8.4	28.0	10	1	AAA11232	RAPD primer U-12 f
c 90	8.4	28.0	10	1	AAH63301	Human colon epithe
91	8.4	28.0	10	1	AAH63452	Human ubiquitously
c 92	8.4	28.0	10	1	AAH64237	Human ubiquitously
c 93	8.4	28.0	10	1	ABA06059	Human normal hepat
94	8.4	28.0	10	1	AAF38816	Yeast NORF gene SA
95	8.4	28.0	10	1	AAF39726	Yeast NORF gene SA
96	8.4	28.0	10	1	AAF40474	Yeast NORF gene SA
97	8.4	28.0	10	1	AAF40855	Yeast NORF gene SA
98	8.4	28.0	10	1	AAF35202	Yeast NORF gene SA
c 99	8.4	28.0	10	1	AAF36577	Yeast NORF gene SA
c 100	8.4	28.0	10	1	AAF36581	Yeast NORF gene SA
101	8.4	28.0	10	1	AAF38900	Yeast NORF gene SA
102	8.4	28.0	10	1	AAF33314	Yeast putative cod
103	8.4	28.0	10	1	AAF34250	Yeast NORF gene SA
c 104	8.4	28.0	10	1	AAF35602	Yeast NORF gene SA
105	8.4	28.0	10	1	AAF38822	Yeast NORF gene SA
c 106	8.4	28.0	10	1	AAF41495	Yeast NORF gene SA

107	8.4	28.0	10	1	AAF34426	Yeast NORF gene SA
c 108	8.4	28.0	10	1	AAF34234	Yeast NORF gene SA
109	8.4	28.0	10	1	AAS19669	Primer-extension o
110	8.4	28.0	10	1	ABL52200	Human PER1 preferr
c 111	8.4	28.0	10	1	ABK81399	SCYA21 gene primer
c 112	8.4	28.0	10	1	ABK96063	Human LIPE gene po
113	8.4	28.0	10	1	AAD25204	Human homeo box D3
c 114	8.4	28.0	10	1	ABV84823	Human haemopexin S
c 115	8.4	28.0	10	1	ABK54423	Human ISL1 gene AS
116	8.4	28.0	10	1	ABK11491	Oligonucleotide pr
117	8.4	28.0	10	1	ABK72629	Leukotriene B4 rec
c 118	8.4	28.0	10	1	ACA94480	DNA tag from human
119	8.4	28.0	10	1	ABT14411	Nucleic acid PCR a
120	8.4	28.0	10	1	ABT14323	Nucleic acid PCR a
c 121	8.4	28.0	11	1	AAX14955	Triple helix third
122	8.4	28.0	11	1	ABQ86554	Human skin stress/
c 123	8.4	28.0	11	1	ABQ86306	Human skin stress/
c 124	8.4	28.0	11	1	ABQ87206	Human skin stress/
c 125	8.4	28.0	11	1	ABV64744	Human skin EST 253
126	8.4	28.0	11	1	ABV67763	Human skin EST 554
127	8.4	28.0	11	1	ABV69450	Human skin EST 723
c 128	8.4	28.0	11	1	ABV69082	Human skin EST 686
c 129	8.4	28.0	11	1	ABV66348	Human skin EST 413
130	8.4	28.0	11	1	ABV66542	Human skin EST 432
131	8.4	28.0	11	1	ABV66760	Human skin EST 454
c 132	8.4	28.0	11	1	ABV68413	Human skin EST 619
c 133	8.4	28.0	11	1	ABV69080	Human skin EST 686
134	8.4	28.0	11	1	ABV68371	Human skin EST 615
135	8.4	28.0	11	1	ABV68621	Human skin EST 640
c 136	8.4	28.0	11	1	ABV63846	Human skin EST 163
137	8.4	28.0	11	1	ABV65219	Human skin EST 300
c 138	8.4	28.0	11	1	ABV66909	Human skin EST 469
c 139	8.4	28.0	11	1	ABV71267	Human skin EST 905
140	8.4	28.0	11	1	ABV67181	Human skin EST 496
c 141	8.4	28.0	11	1	ABV66102	Human skin EST 388
c 142	8.4	28.0	11	1	AAS21210	Transmissible gast
c 143	8.4	28.0	11	1	ABT16435	Human neurokinin 1

ALIGNMENTS

```
RESULT 1
AAQ24060
ID   AAQ24060 standard; RNA; 17 BP.
XX
AC   AAQ24060;
XX
DT   08-JUN-1992  (first entry)
XX
DE   Artificial HIV-1 TAR sequence containing U-rich bubble.
XX
KW   human immunodeficiency virus; tat protein; AIDS; hairpin loop;
KW   trans-activation responsive region; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_structure  5. .12
FT                   /*tag=  a
FT                   /note= "U-rich bubble. Base pairs to nucleotides 6-10 of
FT                   AAQ24061"
XX
PN   WO9202228-A.
XX
PD   20-FEB-1992.
XX
PF   02-AUG-1990;   90GB-00016973.
XX
PR   02-AUG-1990;   90GB-00016973.
XX
PA   (MEDI-) MED RES COUNCIL.
XX
PI   Karn J,  Gait MJ,  Heaphy S,  Dingwall C;
XX
DR   WPI; 1992-079785/10.
XX
PT   New HIV growth inhibiting oligo:nucleotide(s) - comprising rna binding
PT   sequences capable of binding to tat protein within cells, and in assays
PT   to identify cpds. with tat binding.
XX
PS   Disclosure; Fig 18c; 89pp; English.
XX
CC   The HIV-1 TAR stem-loop sequence (see AAQ21425) was compared to that from
CC   HIV-2 (see AAQ21426). The only regions common to the two TAR structures
CC   are in the loop region and the U-rich bubble in the upper stem. This 17-
CC   mer was synthesised and can hybridise to a 14-mer (see AAQ24061) to mimic
CC   the known HIV-1 tat recognition sequence but without the apical loop. In
CC   an assay, the 17-mer plus 14-mer structure competed satisfactorily with
CC   full-length (59-mer) TAR for binding to tat. See AAQ21427-Q21435 for TAR
CC   mutants
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 2
AAZ59070
ID   AAZ59070 standard; RNA; 17 BP.
XX
AC   AAZ59070;
XX
DT   15-SEP-2003  (revised)
DT   11-APR-2000  (first entry)
XX
DE   HIV-1 TAR oligonucleotide target sequence #1.
XX
KW   Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;
KW   fluorescence resonance energy transfer; tat; HIV-1; Rev response element;
KW   autoimmune disease; trans-activation regulatory region; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9964625-A2.
XX
PD   16-DEC-1999.
XX
PF   04-JUN-1999;   99WO-GB001761.
XX
PR   05-JUN-1998;   98GB-00012196.
PR   02-MAR-1999;   99GB-00004790.
XX
PA   (RIBO-) RIBOTARGETS LTD.
XX
PI   Karn J,  Prescott CD;
XX
DR   WPI; 2000-097545/08.
XX
PT   Identifying compounds that bind to target RNA, potentially useful for
PT   treating infections, tumors and autoimmune diseases.
XX
PS   Example; Page 31; 82pp; English.
XX
CC   The invention relates to a method of determining if a compound binds to a
CC   target RNA by treating a test compound with a reporter (R) labelled with
CC   a donor or acceptor group and labelled target RNA, labelled with the
CC   complementary donor or acceptor group, and measuring the fluorescence
CC   from fluorescent groups associated with a compound:target RNA complex in
CC   presence of the test compound and comparing the result with a standard.
```

CC The oligonucleotides AAZ59070-Z59071 anneal to form a double stranded
CC oligonucleotide containing the HIV-1 trans-activation regulatory region
CC (TAR) to which the HIV-1 Tat protein binds. The complex is labelled with
CC 6-carboxyfluorescein and is used as a target for the binding of a
CC labelled ADP-1 protein. Detection of the complex is by fluorescence
CC resonance energy transfer (FRET). The method is used to identify
CC compounds that interfere with interaction between the target RNA and
CC ligands or proteins. Compounds that are identified are potentially useful
CC for treating infections (viral, bacterial or fungal), cancer and
CC autoimmune diseases. The compounds are preferably directed to the TAR and
CC RRE regions of human immunodeficiency virus RNA and inhibit viral
CC replication. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 46.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 9;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1490 AGCCAGACTTCAGCAGC 1506
||||||| :: ||||||
Db 1 AGCCAGAUUUGAGCAGC 17

RESULT 3
ABK26439
ID ABK26439 standard; DNA; 17 BP.
XX
AC ABK26439;
XX
DT 09-APR-2002 (first entry)
XX
DE Waxy starch production genome altering oligonucleotide #95.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Solanum tuberosum.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
PS Claim 7; Page 151; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyric herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 46.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 9;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1485 CAAGAAGCCAGACTTCA 1501
||||||| | ||||||
Db 1 CAAGAAGCTAAACTTCA 17

RESULT 4
ABK26440/c
ID ABK26440 standard; DNA; 17 BP.
XX
AC ABK26440;
XX
DT 09-APR-2002 (first entry)
XX
DE Waxy starch production genome altering oligonucleotide #96.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Solanum tuberosum.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;

```
XX
DR   WPI; 2002-106307/14.
XX
PT   New oligonucleotides with modified nuclease-resistant termini, useful for
PT   creating plants with desired phenotypes, e.g. stress tolerance, improved
PT   nutritional value, herbicide or disease resistance, or modified oil
PT   production.
XX
PS   Claim 7; Page 151; 220pp; English.
XX
CC   The invention relates to an oligonucleotide for targeted alteration of a
CC   genetic sequence, which comprises a single-stranded oligonucleotide
CC   having a DNA domain. The DNA domain has at least one mismatch with
CC   respect to the genetic sequence to be altered and further comprises
CC   chemical modifications of the oligonucleotide. The chemical modifications
CC   consist of o-methyl modification, an LNA modification, two or more
CC   phosphorothioate linkages on a terminus, or a combination of any two or
CC   more of these modifications. The oligonucleotides are useful for
CC   directing repair or alteration of plant genetic information. The
CC   oligonucleotides are particularly useful for creating plants with desired
CC   phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC   nutritional value (e.g. altering amino acid content of plants or
CC   conferring amino acid over production), herbicide resistance (e.g.
CC   glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC   resistance, porphyric herbicide resistance or triazine resistance),
CC   disease resistance, modified oil production, modified starch production
CC   (e.g. increased starch or production of waxy starch), altered floral
CC   morphology (e.g. male-sterile plants) or modified fatty acid content
CC   (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC   The oligonucleotides are also useful for producing albino mutants for the
CC   analysis of photosynthetic processes. This sequence represents a genome
CC   altering oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 3 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 9;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAGACTTCA 1501
              ||||||||  | ||||||
Db         17 CAAGAAGCTAAACTTCA 1


RESULT 5
AAZ59072
ID   AAZ59072 standard; RNA; 18 BP.
XX
AC   AAZ59072;
XX
DT   15-SEP-2003  (revised)
DT   11-APR-2000  (first entry)
XX
DE   HIV-1 TAR oligonucleotide target sequence #3.
XX
KW   Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;
KW   fluorescence resonance energy transfer; tat; HIV-1; Rev response element;
KW   autoimmune disease; trans-activation regulatory region; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9964625-A2.
XX
PD   16-DEC-1999.
XX
PF   04-JUN-1999;   99WO-GB001761.
XX
PR   05-JUN-1998;   98GB-00012196.
PR   02-MAR-1999;   99GB-00004790.
XX
PA   (RIBO-) RIBOTARGETS LTD.
XX
PI   Karn J,  Prescott CD;
XX
DR   WPI; 2000-097545/08.
XX
PT   Identifying compounds that bind to target RNA, potentially useful for
PT   treating infections, tumors and autoimmune diseases.
XX
PS   Example; Page 31; 82pp; English.
XX
CC   The invention relates to a method of determining if a compound binds to a
CC   target RNA by treating a test compound with a reporter (R) labelled with
CC   a donor or acceptor group and labelled target RNA, labelled with the
CC   complementary donor or acceptor group, and measuring the fluorescence
CC   from fluorescent groups associated with a compound:target RNA complex in
CC   presence of the test compound and comparing the result with a standard.
CC   The oligonucleotides AAZ59070-Z59071 anneal to form a double stranded
CC   oligonucleotide containing the HIV-1 trans-activation regulatory region
CC   (TAR) to which the HIV-1 Tat protein binds. The complex is labelled with
CC   6-carboxyfluorescein and is used as a target for the binding of a
CC   labelled ADP-1 protein. Detection of the complex is by fluorescence
CC   resonance energy transfer (FRET). The method is used to identify
CC   compounds that interfere with interaction between the target RNA and
CC   ligands or proteins. Compounds that are identified are potentially useful
CC   for treating infections (viral, bacterial or fungal), cancer and
CC   autoimmune diseases. The compounds are preferably directed to the TAR and
CC   RRE regions of human immunodeficiency virus RNA and inhibit viral
CC   replication. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 18 BP; 5 A; 4 C; 6 G; 0 T; 3 U; 0 Other;

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 9.5;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 6
AAF74454
ID   AAF74454 standard; DNA; 18 BP.
XX
AC   AAF74454;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Human PRO2 gene-specific sequencing primer SEQ ID NO:40.
XX
KW   Human; PRO; PROX; cytostatic; immunomodulatory; reproduction;
KW   gene therapy; cell proliferation; differentiation disorder; cancer;
KW   immune associated disorder; gestational disease; pre-clampsia;
KW   PCR primer; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200110902-A2.
XX
PD   15-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US021857.
XX
PR   11-AUG-1999;   99US-0148433P.
PR   10-AUG-2000; 2000US-00635949.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Fernandes E;
XX
DR   WPI; 2001-147509/15.
XX
PT   Nucleic acids encoding secreted polypeptides, designated PROX
PT   polypeptides, useful for treating a syndrome associated with a PROX-
PT   associated disorder, e.g. cancer.
```

```
XX
PS   Example 2; Page 119; 166pp; English.
XX
CC   The present invention describes isolated nucleic acids encoding secreted
CC   polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where
CC   X is an integer from 1 to 17). PROX polypeptides have cytostatic,
CC   immunomodulatory and reproduction activities, and can be used in gene
CC   therapy, and as PROX antagonists and PROX agonists. PROX polypeptides,
CC   nucleic acids and antibodies are useful in the manufacture of a
CC   medicament for treating a syndrome associated with a PROX-associated
CC   disorder, e.g. a cell proliferation and/or differentiation disorder (e.g.
CC   cancer or immune associated disorders) and a gestational disease (e.g.
CC   pre-clampsia). They are also used for screening for a modulator of
CC   activity or of latency or predisposition to a PROX-associated disorder.
CC   AAF74432 to AAF74448 encode the specifically claimed human PROX
CC   polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547. The present
CC   sequence represents a primer used in an example from the present
CC   invention
XX
SQ   Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 9.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
              | ||||||||||||| |
Db          2 CTACCAAGAAGCCAGCC 18


RESULT 7
AAF74457/c
ID   AAF74457 standard; DNA; 18 BP.
XX
AC   AAF74457;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Human PRO2 gene-specific sequencing primer SEQ ID NO:43.
XX
KW   Human; PRO; PROX; cytostatic; immunomodulatory; reproduction;
KW   gene therapy; cell proliferation; differentiation disorder; cancer;
KW   immune associated disorder; gestational disease; pre-clampsia;
KW   PCR primer; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200110902-A2.
XX
PD   15-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US021857.
XX
PR   11-AUG-1999;   99US-0148433P.
PR   10-AUG-2000; 2000US-00635949.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Fernandes E;
XX
DR   WPI; 2001-147509/15.
XX
PT   Nucleic acids encoding secreted polypeptides, designated PROX
PT   polypeptides, useful for treating a syndrome associated with a PROX-
PT   associated disorder, e.g. cancer.
XX
PS   Example 2; Page 119; 166pp; English.
XX
CC   The present invention describes isolated nucleic acids encoding secreted
CC   polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where
CC   X is an integer from 1 to 17). PROX polypeptides have cytostatic,
CC   immunomodulatory and reproduction activities, and can be used in gene
CC   therapy, and as PROX antagonists and PROX agonists. PROX polypeptides,
CC   nucleic acids and antibodies are useful in the manufacture of a
CC   medicament for treating a syndrome associated with a PROX-associated
CC   disorder, e.g. a cell proliferation and/or differentiation disorder (e.g.
CC   cancer or immune associated disorders) and a gestational disease (e.g.
CC   pre-clampsia). They are also used for screening for a modulator of
CC   activity or of latency or predisposition to a PROX-associated disorder.
CC   AAF74432 to AAF74448 encode the specifically claimed human PROX
CC   polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547. The present
CC   sequence represents a primer used in an example from the present
CC   invention
XX
SQ   Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 9.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
              | ||||||||||||| |
Db          17 CTACCAAGAAGCCAGCC 1


RESULT 8
AAX57566
ID   AAX57566 standard; DNA; 15 BP.
XX
AC   AAX57566;
XX
DT   16-JUL-1999  (first entry)
XX
DE   Antisense oligo #5 to insulin-like growth factor I receptor.
XX
KW   Antisense; human; insulin-like growth factor-1 receptor; IGF-1R;
KW   expression; inhibition; induction; apoptosis; tumour; liposome; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9923259-A1.
XX
PD   14-MAY-1999.
XX
PF   03-NOV-1998;   98WO-US023418.
XX
PR   04-NOV-1997;   97US-00963886.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Zon G;
XX
DR   WPI; 1999-313361/26.
XX
PT   Human insulin-like growth factor-1 receptor gene antisense
PT   oligonucleotides.
XX
PS   Disclosure; Page 16; 23pp; English.
XX
CC   Sequences AAX57562-X57571 represent antisense oligonucleotides targeted
CC   to a region spanning 4-9 codons downstream of the AUG translation
CC   initiation codon of the human insulin-like growth factor-1 receptor (IGF-
CC   1R) gene. The antisense oligonucleotides inhibit the expression of IGF-
CC   1R, which in turn induces apoptosis, especially in a tumour cell. The
CC   oligonucleotides can be administered via a liposome
XX
SQ   Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             41.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 15;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTCA 1501
              | ||||||||||||
Db          1 GGAGCCAGACTTCA 14
```

```
RESULT 9
AAF49086/c
ID   AAF49086 standard; DNA; 15 BP.
XX
AC   AAF49086;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #46.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 61; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             41.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 15;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTCA 1501
              | ||||||||||||
Db         15 GGAGCCAGACTTCA 2


RESULT 10
AAF49087/c
ID   AAF49087 standard; DNA; 15 BP.
XX
AC   AAF49087;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #47.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 61; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             41.3%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 15;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTCA 1501
              | ||||||||||||
Db         14 GGAGCCAGACTTCA 1


RESULT 11
AAZ64832/c
ID   AAZ64832 standard; RNA; 14 BP.
XX
AC   AAZ64832;
XX
```

DT 28-MAR-2000 (first entry)
XX
DE Substrate for hairpin ribozyme which cleaves HCV at nt. 6599.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
DR WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 2; Page 99; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
CC Hepatitis C virus (HCV) RNA sequence at the base position given in the
CC descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 14 BP; 3 A; 2 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 40.0%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGCCA 1508
||||||||||||
Db 12 CTTCAGCAGCCA 1

RESULT 12
ABX01669/c
ID ABX01669 standard; RNA; 14 BP.
XX
AC ABX01669;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #154 for HCV hairpin ribozyme #154.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hairpin ribozyme; HP ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 2; Page 62; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 14 BP; 3 A; 2 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 40.0%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGCCA 1508
||||||||||||
Db 12 CTTCAGCAGCCA 1

RESULT 13
AAF49084/c
ID AAF49084 standard; DNA; 15 BP.
XX
AC AAF49084;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #44.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 61; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1490 AGCCAGACTTCA 1501
             ||||||||||||
Db         15 AGCCAGACTTCA 4
```

RESULT 14
AAF49085/c
ID AAF49085 standard; DNA; 15 BP.
XX
AC AAF49085;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #45.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 61; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1490 AGCCAGACTTCA 1501
             ||||||||||||
Db         14 AGCCAGACTTCA 3
```

RESULT 15
AAT49619/c
ID AAT49619 standard; RNA; 15 BP.
XX
AC AAT49619;
XX
DT 28-FEB-1997 (first entry)
XX
DE Human CETP HH ribozyme target sequence #477.
XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX

PF 11-DEC-1995; 95WO-US016000.
XX
PR 23-DEC-1994; 94US-00363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
PS Claim 4; Page 29; 72pp; English.
XX
CC AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence UH
CC is immediately upstream. The ribozymes are able to cleave mRNA from the
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 4 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 39.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1488 GAAGCCAGACTTCAG 1502
              | ||||| |||||||
Db         15 GTAGCCATACTTCAG 1
```

RESULT 16
AAF47839
ID AAF47839 standard; DNA; 15 BP.
XX
AC AAF47839;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1259.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 52; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 5 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 39.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1487 AGAAGCCAGACTTCA 1501
              || | ||||||||||
Db          1 AGCACCCAGACTTCA 15
```

RESULT 17
AAX57564
ID AAX57564 standard; DNA; 15 BP.
XX
AC AAX57564;
XX
DT 16-JUL-1999 (first entry)
XX
DE Antisense oligo #3 to insulin-like growth factor I receptor.
XX
KW Antisense; human; insulin-like growth factor-1 receptor; IGF-1R;
KW expression; inhibition; induction; apoptosis; tumour; liposome; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9923259-A1.
XX
PD 14-MAY-1999.
XX
PF 03-NOV-1998; 98WO-US023418.
XX
PR 04-NOV-1997; 97US-00963886.
XX
PA (INEX-) INEX PHARM CORP.

XX
PI Zon G;
XX
DR WPI; 1999-313361/26.
XX
PT Human insulin-like growth factor-1 receptor gene antisense
PT oligonucleotides.
XX
PS Disclosure; Page 15; 23pp; English.
XX
CC Sequences AAX57562-X57571 represent antisense oligonucleotides targeted
CC to a region spanning 4-9 codons downstream of the AUG translation
CC initiation codon of the human insulin-like growth factor-1 receptor (IGF-
CC 1R) gene. The antisense oligonucleotides inhibit the expression of IGF-
CC 1R, which in turn induces apoptosis, especially in a tumour cell. The
CC oligonucleotides can be administered via a liposome
XX
SQ Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.0%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1488 GAAGCCAGACTTC 1500
| ||||||||||||
Db 3 GGAGCCAGACTTC 15

RESULT 18
AAZ35973
ID AAZ35973 standard; DNA; 15 BP.
XX
AC AAZ35973;
XX
DT 09-FEB-2000 (first entry)
XX
DE Histoplasma capsulatum M antigen degenerate PCR primer M4F.
XX
KW Histoplasma capsulatum; fungus; M antigen; vaccine; detection;
KW histoplasmosis; diagnosis; infection; antimicrobial; antibody;
KW PCR primer; ss.
XX
OS Synthetic.
OS Ajellomyces capsulatus.
XX
PN WO9955874-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009151.
XX
PR 30-APR-1998; 98US-0083676P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Zancope-Oliveira RM, Lott TJ, Mayer LW, Reiss E, Deepe GS;
XX
DR WPI; 2000-023360/02.
XX
PT New isolated Histoplasma capsulatum nucleic acids, used to develop
PT products for the diagnosis, prevention and treatment of histoplasmosis.
XX
PS Example 1; Page 49; 75pp; English.
XX
CC The present sequence represents a degenerate PCR primer for the M antigen
CC isolated from Histoplasma capsulatum (HC). HC polypeptides can be used
CC for detecting antibodies for detecting a previous or current HC infection
CC in a subject. They can also be injected into the skin of a subject to
CC detect past exposure to HC by detecting swelling of the skin. The
CC antibodies can be used for detecting current HC infection in a subject.
CC HC nucleic acids and polypeptides can also be used for the treatment of
CC histoplasmosis as well as in vaccines for the prevention of
CC histoplasmosis
XX
SQ Sequence 15 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 5 Other;

Query Match 38.0%; Score 11.4; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1486 AAGAAGCCAGACTTC 1500
||:|| ||:||:||:
Db 1 AARAAYCCVGAYTTY 15

RESULT 19
AAF49088/c
ID AAF49088 standard; DNA; 15 BP.
XX
AC AAF49088;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #48.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST..
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 61; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 38.0%; Score 11.4; DB 1; Length 15;

```
  Best Local Similarity   92.3%;  Pred. No. 23;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTC 1500
              | ||||||||||||
Db         13 GGAGCCAGACTTC 1
```

RESULT 20
AAZ64816/c
ID   AAZ64816 standard; RNA; 14 BP.
XX
AC   AAZ64816;
XX
DT   28-MAR-2000 (first entry)
XX
DE   Substrate for hairpin ribozyme which cleaves HCV at nt. 5792.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 2; Page 98; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
CC   Hepatitis C virus (HCV) RNA sequence at the base position given in the
CC   descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 14 BP; 2 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

```
  Query Match             36.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 27;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAGCCA 1508
              || || ||||||||
Db         14 GAGTTGAGCAGCCA 1
```

RESULT 21
AAA99958/c
ID   AAA99958 standard; DNA; 14 BP.
XX
AC   AAA99958;
XX
DT   15-SEP-2003 (revised)
DT   25-JAN-2001 (first entry)
XX
DE   Geminivirus Rep repeat motif sequence #3.
XX
KW   Geminivirus; replication associated protein; rep; iteron; antagonists;
KW   plant; ss.
XX
OS   Geminiviridae.
XX
PN   WO200043494-A2.
XX
PD   27-JUL-2000.
XX
PF   27-JAN-2000; 2000WO-US001849.
XX
PR   26-JAN-1999;   99US-0117285P.
XX
PA   (SCRI) SCRIPPS RES INST.
XX
PI   Fauquet C, Chatterji A;
XX
DR   WPI; 2000-499224/44.
XX
PT   Producing plants resistant to geminivirus, and inhibiting geminivirus
PT   replication in plants, by introducing replication associated protein
PT   iteron antagonists into the plant, plant cells or propagules.
XX
PS   Example 1; Page 51; 172pp; English.
XX
CC   The present invention relates to methods for producing plants resistant
CC   to geminivirus, involving introducing a geminivirus replication
CC   associated protein (Rep)-iteron antagonist into a plant. The antagonist
CC   is a nucleotide sequence of a geminivirus iteron capable of binding to a
CC   Rep protein or a defective Rep which has a conserved geminivirus iteron
CC   binding site. The present sequence is a geminivirus Rep repeat motif
CC   sequence. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 14 BP; 1 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

```
  Query Match             36.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 27;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGACTTC 1500
              ||| |||||||| |
Db         14 AGACGCCAGACTCC 1
```

RESULT 22
ABX01653/c
ID   ABX01653 standard; RNA; 14 BP.
XX
AC   ABX01653;
XX
DT   23-DEC-2002 (first entry)
XX
DE   Hepatitis C virus substrate #138 for HCV hairpin ribozyme #138.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hairpin ribozyme; HP ribozyme; ss.
XX
OS   Hepatitis C virus.

XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 2; Page 62; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 14 BP; 2 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 36.0%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1495 GACTTCAGCAGCCA 1508
|| || ||||||||
Db 14 GAGTTGAGCAGCCA 1

RESULT 23
ABF18234/c
ID ABF18234 standard; DNA; 13 BP.
XX
AC ABF18234;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 118231 for detecting SNP TSC0029560.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 118231; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 1 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 34.7%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CACGACCAAGAA 1490
|||||||| ||
Db 13 CACGACCAAAAA 2

RESULT 24
ABF18235
ID ABF18235 standard; DNA; 13 BP.
XX
AC ABF18235;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 118232 for detecting SNP TSC0029560.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

```
XX
PS   Claim 1; SEQ ID NO 118232; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 7 A; 5 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             34.7%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 30;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAGAA 1490
              ||||||||| ||
Db          1 CACGACCAAAAA 12


RESULT 25
AAZ78899
ID   AAZ78899 standard; DNA; 10 BP.
XX
AC   AAZ78899;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1327.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 103; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              ||||||||||
Db          1 AGAAGCCAGA 10


RESULT 26
AAZ83653/c
ID   AAZ83653 standard; DNA; 10 BP.
XX
AC   AAZ83653;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2887.
```

```
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 136; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCAG 1505
              ||||||||||
Db         10 ACTTCAGCAG 1

RESULT 27
AAF39527
ID   AAF39527 standard; DNA; 10 BP.
XX
AC   AAF39527;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6266.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 223; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              ||||||||||
Db          1 AGAAGCCAGA 10

RESULT 28
AAF34162
ID   AAF34162 standard; DNA; 10 BP.
XX
```

AC AAF34162;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:901.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 32; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 33.3%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1486 AAGAAGCCAG 1495
||||||||||
Db 1 AAGAAGCCAG 10

RESULT 29
AAF39463
ID AAF39463 standard; DNA; 10 BP.
XX
AC AAF39463;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6202.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 221; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1496 ACTTCAGCAG 1505
||||||||||
Db 1 ACTTCAGCAG 10

```
RESULT 30
AAF41899
ID   AAF41899 standard; DNA; 10 BP.
XX
AC   AAF41899;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8638.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 308; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1482 GACCAAGAAG 1491
             ||||||||||
Db          1 GACCAAGAAG 10


RESULT 31
AAV32260/c
ID   AAV32260 standard; DNA; 12 BP.
XX
AC   AAV32260;
XX
DT   18-AUG-1998  (first entry)
XX
DE   Random primed reverse transcription PCR primer 108.
XX
KW   RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
KW   differential gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO9813521-A1.
XX
PD   02-APR-1998.
XX
PF   26-SEP-1997;   97WO-EP005290.
XX
PR   27-SEP-1996;   96GB-00020216.
XX
PA   (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX
PI   Consalez G,  Fesce R;
XX
DR   WPI; 1998-230725/20.
XX
PT   Differential screening of gene expression by reverse transcription
PT   polymerase chain reaction - uses random priming with primers selected for
PT   high efficiency and selectivity by computer screening of database(s).
XX
PS   Claim 9; Page 24; 37pp; English.
XX
CC   The invention provides a method for the differential screening of gene
CC   expression by random primed reverse transcription PCR (RT-PCR). The
CC   primer sequences are generated by stimulating PCR reactions on non-
CC   redundant mammalian nucleotide sequence databank entries containing at
CC   least 1,000 bp of coding region. The primers selected, such as the
CC   present one, had to meet various criteria such as having an efficiency
CC   index between 2-10, having a selectivity index higher than 1, being 12 bp
CC   long i.e. 8 C or G and 4 T or A, and each primer differed from the others
CC   in at least 5 of the 8 bases at the 3'-end. The invention claims the
CC   selected primers make it possible to use internally primed, PCR-based RNA
CC   fingerprinting for simple, exhaustive and systematic analysis of
CC   differential gene expression as an advantageous alternative to
CC   differential display. The method can also be useful for isolating new
CC   coding sequences and to compare known and new genes
XX
SQ   Sequence 12 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             33.3%;  Score 10;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAG 1488
             ||||||||||
Db         10 CACGACCAAG 1


RESULT 32
AAX89228
ID   AAX89228 standard; DNA; 13 BP.
XX
AC   AAX89228;
XX
DT   15-SEP-1999  (first entry)
```

XX
DE PCR primer H-AP34.
XX
KW ST2L; extracellular domain; mouse; epitope; antibody; T-helper cell; Th1;
KW Th2; medicament; therapy; allergic reaction; asthma; Leishmania;
KW intracellular pathogen; inflammatory disease; arthritis; immunoglobulin;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9934217-A1.
XX
PD 08-JUL-1999.
XX
PF 24-DEC-1998; 98WO-GB003913.
XX
PR 24-DEC-1997; 97GB-00027172.
XX
PA (UNIU) UNIV GLASGOW.
XX
PI Liew FY, Xu D;
XX
DR WPI; 1999-430265/36.
XX
PT Novel antibody to ST2L, an epitope found on the extracellular surfaces of
PT T helper 1 cells.
XX
PS Disclosure; Page 12; 44pp; English.
XX
CC The invention provides an antibody specific for epitopes (AAY27164-175)
CC located on the extracellular domain of ST2L protein. The antibody is
CC used: (a) in a binding assay to identify and/or distinguish T-helper 1
CC (Th1) or Th2 and evaluate the abundance of Th2 in a sample of body fluid
CC or tissue; (b) to lyse Th2 cells in preference to Th1 cells or otherwise
CC inhibit Th2 cell function; and (c) as a medicament for use in therapy as
CC a mediator of an allergic reaction, e.g. asthma; diseases mediated by
CC intracellular pathogens, especially Leishmania, or against an
CC inflammatory disease, especially arthritis. The antibody is targeted to
CC an epitope (ST2L) which is a member of the immunoglobulin superfamily and
CC is found on Th2 cells and not Th1 cells
XX
SQ Sequence 13 BP; 4 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGC 1506
||||||||||
Db 4 CTTCAGCAGC 13

RESULT 33
ADC64953
ID ADC64953 standard; DNA; 13 BP.
XX
AC ADC64953;
XX
DT 18-DEC-2003 (first entry)
XX
DE Camellia sinensis L. (O.) Kuntze related PCR primer AP34.
XX
KW Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS Synthetic.
OS Camellia sinensis.
XX
PN CN1377966-A.
XX
PD 06-NOV-2002.
XX
PF 30-MAR-2001; 2001CN-00112459.
XX
PR 30-MAR-2001; 2001CN-00112459.
XX
PA (SCIN-) SCI & IND RES COMMISSION.
XX
DR WPI; 2003-230959/23.
XX
PT Cloning of a new gene sequence expressed and inhibited during winter
PT dormancy of a tea tree top plumelet, comprises identification, cloning
PT and analysis of a new primer in the gene sequence.
XX
PS Example 3; Page 32; 66pp; Chinese.
XX
CC The present invention describes the cloning of a new gene sequence
CC expressed and inhibited during hibernation of the top plumelet of a
CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC identification, cloning and analysis of a primer terminal in the gene
CC sequence expressed and inhibited during hibernation of the top plumelet
CC of the tea tree. The present sequence represents a PCR primer which is
CC used in an example from the present invention.
XX
SQ Sequence 13 BP; 4 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGC 1506
||||||||||
Db 4 CTTCAGCAGC 13

RESULT 34
ABH65692/c
ID ABH65692 standard; DNA; 13 BP.
XX
AC ABH65692;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 265669 for detecting SNP TSC0064388.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 265669; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

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CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             32.7%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 39;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTTCA 1501
              || ||| ||||||
Db         13 AACCCATACTTCA 1


RESULT 35
ABH65694/c
ID   ABH65694 standard; DNA; 13 BP.
XX
AC   ABH65694;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 265671 for detecting SNP TSC0064388.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 265671; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             32.7%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 39;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTTCA 1501
              || ||| ||||||
Db         13 AACCCAAACTTCA 1


RESULT 36
ABH65693
ID   ABH65693 standard; DNA; 13 BP.
XX
AC   ABH65693;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 265670 for detecting SNP TSC0064388.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 265670; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             32.7%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 39;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTTCA 1501
              || ||| ||||||
Db          1 AACCCATACTTCA 13


RESULT 37
ABH65695
ID   ABH65695 standard; DNA; 13 BP.
XX
AC   ABH65695;
XX
DT   22-FEB-2002  (first entry)
XX
```

```
DE   Oligonucleotide SEQ ID NO 265672 for detecting SNP TSC0064388.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 265672; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             32.7%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 39;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTTCA 1501
              || ||| ||||||
Db          1 AACCCAAACTTCA 13


RESULT 38
ABQ83680/c
ID   ABQ83680 standard; DNA; 13 BP.
XX
AC   ABQ83680;
XX
DT   27-JAN-2003  (first entry)
XX
DE   DNA-templated synthesis related oligonucleotide #39.
XX
KW   Molecular function; diversification; selection; amplification; evolve;
KW   synthesis; library; chemical compound; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   WO200274929-A2.
XX
PD   26-SEP-2002.
XX
PF   19-MAR-2002; 2002WO-US008546.
XX
PR   19-MAR-2001; 2001US-0277081P.
PR   19-MAR-2001; 2001US-0277094P.
PR   20-JUL-2001; 2001US-0306691P.
PR   19-MAR-2002; 2002US-00101030.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Liu DR,  Gartner ZJ,  Kanan MW;
XX
DR   WPI; 2002-740858/80.
XX
PT   Synthesizing chemical compounds by hybridizing one or more templates
PT   which have associated reactive unit, with one or more transfer units
PT   having anti-codon and reactive unit, and performing reaction of reactive
PT   units.
XX
PS   Example 5; Fig 32; 146pp; English.
XX
CC   The present invention describes a method (M1) for synthesising one or
CC   more chemical compounds. M1 involves providing one or more templates,
CC   which optionally have a reactive unit associated with them; and
CC   contacting one or more transfer units having an anti-codon and reactive
CC   unit with the one or more templates under conditions to allow for
CC   hybridisation of the one or more anti-codons to template, and reaction of
CC   the reactive units. Also described: (1) a method (M2) of evolving a
CC   library of compounds; (2) a kit comprising one or more nucleic acid
CC   templates and one or more transfer units; (3) a method (M3) for
CC   synthesising one or more non-natural polymers; and (4) a library (I)
CC   comprising one or more chemical compounds where each of the chemical
CC   compounds is bonded to an amplifiable template whose nucleotide sequence
CC   is informative of the structure of the chemical compounds, where the
CC   library is synthesised by M1 or M3. The method can be used for
CC   synthesising one or more chemical compounds which contain an anti-codon
CC   comprising a nucleotide sequence which hybridises with one or more
CC   nucleic acid templates. M1 is useful for synthesising a library of
CC   chemical compounds. The methods are useful for synthesising chemical
CC   compounds that are not, or do not resemble nucleic acids or nucleic acid
CC   analogues. The present sequence represents an oligonucleotide which is
CC   used in an example from the present invention
XX
SQ   Sequence 13 BP; 3 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             32.7%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 39;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1491 GCCAGACTTCAGC 1503
              | |||| ||||||
Db         13 GGCAGATTTCAGC 1


RESULT 39
ABV70346/c
ID   ABV70346 standard; cDNA; 11 BP.
XX
AC   ABV70346;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8132.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
```

PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 259; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

```
  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAG 1505
              |||| ||||||
Db         11 GACTACAGCAG 1
```

RESULT 40
ABV69357/c
ID ABV69357 standard; cDNA; 11 BP.
XX
AC ABV69357;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7143.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 224; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

```
  Query Match             31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAG 1495
              ||||||| |||
Db         11 CAAGAAGGCAG 1
```

RESULT 41
ABV62925/c
ID ABV62925 standard; cDNA; 11 BP.
XX
AC ABV62925;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 711.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 45; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention

```
XX
SQ   Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAG 1505
              |||| ||||||
Db         11 GACTACAGCAG 1


RESULT 42
ABV68643/c
ID   ABV68643 standard; cDNA; 11 BP.
XX
AC   ABV68643;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6429.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 204; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTT 1499
              ||||||| |||
Db         11 AAGCCAGTCTT 1


RESULT 43
ABV69164
ID   ABV69164 standard; cDNA; 11 BP.
XX
AC   ABV69164;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6950.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 218; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 7 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match            31.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity  90.9%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAGA 1496
              ||||||| |||
Db          1 AAGAAGCAAGA 11


RESULT 44
AAZ41704/c
ID   AAZ41704 standard; DNA; 12 BP.
XX
AC   AAZ41704;
XX
DT   20-MAR-2003  (revised)
DT   21-JAN-2000  (first entry)
XX
DE   Organic material detecting primer 65.
XX
KW   Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW   detection; pollutant; soil; food; agricultural chemical; polymer;
KW   organochlorine; primer; ss.
```

XX
OS Synthetic.
XX
PN DE19914461-A1.
XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99DE-01014461.
XX
PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
PT Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
PS Example 1; Page 18; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-Z41855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 31.3%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCCA 1494
||||||.||||
Db 11 CCAAGAGGCCA 1

RESULT 45
AAZ41488/c
ID AAZ41488 standard; DNA; 12 BP.
XX
AC AAZ41488;
XX
DT 19-JAN-2000 (first entry)
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #65.
XX
KW Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11276176-A.
XX
PD 12-OCT-1999.
XX
PF 31-MAR-1998; 98JP-00087652.
XX
PR 31-MAR-1998; 98JP-00087652.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 1999-626940/54.
XX
PT Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
XX
PS Example; Page 9; 40pp; Japanese.
XX
CC A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC organic waste
XX
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 31.3%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCCA 1494
||||||.||||
Db 11 CCAAGAGGCCA 1

RESULT 46
AAC97839/c
ID AAC97839 standard; DNA; 12 BP.
XX
AC AAC97839;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 65.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 2001-011047/02.
XX
PT Amplification of a DNA fragment and its apparatus.
XX
PS Example 1; Page 8; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the

```
CC   invention
XX
SQ   Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 43;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                ||||||  ||||
Db         11 CCAAGAGGCCA 1

RESULT 47
ABI02085/c
ID   ABI02085 standard; DNA; 12 BP.
XX
AC   ABI02085;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 302058 for detecting SNP TSC0019774.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 302058; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 43;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGAA 1490
                ||||||||  ||
Db         12 ACGACCAACAA 2

RESULT 48
ABH84038
ID   ABH84038 standard; DNA; 12 BP.
XX
AC   ABH84038;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 284031 for detecting SNP TSC0011630.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 284031; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 43;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGAA 1490
                ||||||||  ||
Db          1 ACGACCAAAAA 11

RESULT 49
ABI53669/c
ID   ABI53669 standard; DNA; 12 BP.
XX
AC   ABI53669;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 353642 for detecting SNP TSC0048625.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 353642; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 31.3%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1480 ACGACCAAGAA 1490
||||||| ||
Db 12 ACGACCAAAAA 2

RESULT 50
AAI99727/c
ID AAI99727 standard; DNA; 12 BP.
XX
AC AAI99727;
XX
DT 21-JAN-2002 (first entry)
XX
DE Microbial SSC-PCR primer SEQ ID NO 10.
XX
KW PCR primer; microbe; composted waste; soil; contaminant; mercury;
KW arsenic; dioxin; hormone; SSC-PCR; ss.
XX
OS Synthetic.
XX
PN WO200175156-A1.
XX
PD 11-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-JP002516.
XX
PR 31-MAR-2000; 2000JP-00099482.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 2001-662977/76.
XX
PT Microbe identification comprises comparing results of SSC-PCR with a
PT reference database for determining microbial spectrum in soil and compost
PT samples.
XX
PS Example; Page 34; 97pp; Japanese.
XX
CC The invention relates to identification of microbes, especially for
CC obtaining information on the microbial spectrum in composted wastes and
CC in the soil to which they are to be applied, and especially to give an
CC indication of possible contaminants in the soil (such as mercury,
CC arsenic, dioxins and environmental hormones) by the presence of
CC microorganisms associated with them, comprising: (a) polymerase chain
CC reaction on DNA of a mixture of microbes using a number of primers of
CC different amplification probability (SSC-PCR); (b) electrophoresis of the
CC DNA amplification fragments; (c) detecting the bands obtained on the
CC electrophoresis image; (d) correcting errors in the image gradients; (e)
CC measuring the position and intensity of the bands; (f) analyzing the
CC results and creating a list of the band data; (g) searching this list
CC against a reference database ; and (h) displaying the result of the
CC search. The present sequence is that of a PCR primer, useful to the
CC invention
XX
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 31.3%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCCA 1494
|||||| ||||
Db 11 CCAAGAGGCCA 1

RESULT 51
AAX18642/c
ID AAX18642 standard; DNA; 10 BP.
XX
AC AAX18642;
XX
DT 06-MAY-1999 (first entry)
XX
DE p53 serial analysis of gene expression tag #45.
XX
KW p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;
KW rat embryo fibroblast; REF; tumour suppressor; cell cycle control;
KW tumourigenesis; diagnosis; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9901581-A1.
XX
PD 14-JAN-1999.
XX
PF 02-JUL-1998; 98WO-US013903.
XX
PR 02-JUL-1997; 97US-0051573P.
XX
PA (GENZ) GENZYME CORP.
XX
PI Madden SL, Galella EA, Bertelsen AH, Beaudry GA;
XX
DR WPI; 1999-106079/09.
XX
PT Diagnosis of cancer in potentially neoplastic samples - by comparing the
PT level of transcription between RNA transcripts in two tissue samples,
PT useful for providing an extensive profile of gene expression in rat
PT embryo fibroblast (REF) cells.
XX

```
PS   Example 2; Page 16; 32pp; English.
XX
CC   A method has been developed for the diagnosis of cancer in potentially
CC   neoplastic samples. The method comprises comparing the level of
CC   transcription between RNA transcripts in two tissue samples (which are of
CC   the same type), where the first sample is potentially neoplastic, and the
CC   second sample is normal human tissue. The first sample is categorized as
CC   neoplastic if its level of transcription is lower than that of the second
CC   sample. The transcript is selected from Alu, RAS, U6 snRNA, 16S RNA, EGR-
CC   1, ribosomal protein S27, ETS-1, 28S RNA, CGR11, and LIMK-2, and it is
CC   identified by a tag selected from ribosomal protein L13a, alpha-tubulin
CC   (T1) and (T2), thymosin beta-4, and gamma- actin. The present sequence
CC   represents a serial analysis of gene expression (SAGE) tag from the
CC   present invention. The use of SAGE tags provides an extensive profile of
CC   gene expression in rat embryo fibroblast (REF) cells containing the (non)
CC   -functional p53 tumour suppression gene. The discovery of new SAGE tags,
CC   which are regulated by p53, enables the diagnosis of genes that are
CC   related to cell cycle control and tumourigenesis
XX
SQ   Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 52
AAZ79219/c
ID   AAZ79219 standard; DNA; 10 BP.
XX
AC   AAZ79219;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1647.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 112; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 53
AAZ83241/c
ID   AAZ83241 standard; DNA; 10 BP.
XX
AC   AAZ83241;
XX
```

```
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2475.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 126; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 54
AAZ83053/c
ID   AAZ83053 standard; DNA; 10 BP.
XX
AC   AAZ83053;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2287.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 120; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         10 CAGCAGCCA 2


RESULT 55
AAZ86659
```

```
ID   AAZ86659 standard; DNA; 10 BP.
XX
AC   AAZ86659;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5893.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 213; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCA 1494
              |||||||||
Db          2 AAGAAGCCA 10
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```
RESULT 56
AAA15242
ID   AAA15242 standard; DNA; 10 BP.
XX
AC   AAA15242;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Primer MR7 for modified differential display of tumour antigens.
XX
KW   Epitope; tumour specific epitope; antigen; vaccine; tumour regression;
KW   cancer; infection; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200028016-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1998;   98WO-US024029.
XX
PR   10-NOV-1998;   98WO-US024029.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Zauderer M;
XX
DR   WPI; 2000-376533/32.
XX
PT   Novel method of identifying target epitopes or antigens specific for
PT   human tumors, cancers and infected cells involving screening expression
PT   library products of a cell expressing the target epitope.
XX
PS   Disclosure; Page 68; 132pp; English.
XX
CC   AAA15239-50 represent arbitrary primers which are used for modified
CC   differential display of tumour antigens, in the method of the invention.
CC   The specification describes a method for identifying a target epitope.
CC   The method comprises screening the products of an expression library from
CC   a cell expressing the target epitope with cytotoxic T cells generated
CC   against the cell to identify DNA clones expressing the target epitope.
CC   The method may also comprise providing a cytotoxic T cell specific for a
CC   gene product differentially expressed by a cell and measuring the cross-
CC   reactivity of the cytotoxic T cell. The methods are useful for
CC   identifying tumour specific target epitopes and antigens which are useful
CC   in immunogenic compositions or vaccines to induce the regression of
CC   tumors, cancers or infections in mammals. The genes expressed in a panel
CC   of tumour cells that are derived from single immortalised, non-
CC   tumourigenic cell line are used to generate HLA restricted cytotoxic T
CC   cells which are evaluated for activity against tumour cells. The method
CC   is useful to identify potential antigens expressed not only by the
CC   pathogen but also by the host cells whose gene expression is altered as a
CC   result of infection. The differential gene expression strategies can be
CC   applied to identify immunogenic molecules of cells infected with virus,
CC   fungus or mycobacterium
XX
SQ   Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
              |||||||||
Db          2 CAGACTTCA 10


RESULT 57
AAF70127/c
ID   AAF70127 standard; DNA; 10 BP.
XX
AC   AAF70127;
XX
```

DT 18-APR-2001 (first entry)
XX
DE Human TNFRSF11B gene primer-extension oligo, SEQ ID NO: 183.
XX
KW Human; TNFRSF11B; osteoclastogenesis inhibitory factor;
KW single nucleotide polymorphism; SNP; osteoclast recruitment;
KW osteoclast function; osteoporosis; metastatic bone disease;
KW Paget's disease; rheumatoid arthritis; periodontal bone disease;
KW primer extension; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200104137-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018803.
XX
PR 09-JUL-1999; 99US-0143020P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-147175/15.
XX
PT Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising single
PT nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's
PT disease and rheumatoid arthritis.
XX
PS Disclosure; Page 24; 114pp; English.
XX
CC The present sequence is a primer used to detect polymorphisms in the
CC human osteoclastogenesis inhibitory factor (TNFRSF11B). Polynucleotides
CC comprising one or more of twenty four novel single nucleotide
CC polymorphisms in the TNFRSF11B gene have been identified. TNFRSF11B
CC regulate osteoclast recruitment and function. An understanding of
CC variations in the gene should thus be useful in developing new therapies
CC for metabolic disorders caused by abnormal osteoclast recruitment and
CC function such as osteoporosis, metastatic bone disease, Paget's disease,
CC rheumatoid arthritis and periodontal bone disease
XX
SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1496 ACTTCAGCA 1504
||||||||| |
Db 9 ACTTCAGCA 1

RESULT 58
AAF35009/c
ID AAF35009 standard; DNA; 10 BP.
XX
AC AAF35009;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1748.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 62; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1498 TTCAGCAGC 1506
||||||||| |
Db 10 TTCAGCAGC 2

RESULT 59
AAF39472/c
ID AAF39472 standard; DNA; 10 BP.
XX
AC AAF39472;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6211.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX

PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 221; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1483 ACCAAGAAG 1491
||||||||| |
Db 10 ACCAAGAAG 2

RESULT 60
AAF38820
ID AAF38820 standard; DNA; 10 BP.
XX
AC AAF38820;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5559.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 198; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1486 AAGAAGCCA 1494
||||||||| |
Db 1 AAGAAGCCA 9

RESULT 61
AAF41980
ID AAF41980 standard; DNA; 10 BP.
XX
AC AAF41980;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8719.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

```
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 311; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAG 1495
              |||||||||
Db          2 AGAAGCCAG 10


RESULT 62
AAF38821
ID   AAF38821 standard; DNA; 10 BP.
XX
AC   AAF38821;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5560.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 198; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCA 1494
              |||||||||
Db          1 AAGAAGCCA 9


RESULT 63
AAF39528
ID   AAF39528 standard; DNA; 10 BP.
XX
AC   AAF39528;
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XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6267.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 223; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAG 1495
              |||||||||
Db          1 AGAAGCCAG 9


RESULT 64
AAF38557
ID   AAF38557 standard; DNA; 10 BP.
XX
AC   AAF38557;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5296.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 189; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGAC 1497
              |||||||||
Db          2 AAGCCAGAC 10
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RESULT 65
AAD31785
ID   AAD31785 standard; DNA; 10 BP.
XX
AC   AAD31785;
XX
DT   18-JUN-2002  (first entry)
XX
DE   MR 7 arbitrary primer used for modified differential display.
XX
KW   Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW   vaccine; immune response; cytostatic; primer; ss.
XX
OS   Unidentified.
XX
PN   US2002018785-A1.
XX
PD   14-FEB-2002.
XX
PF   02-APR-2001; 2001US-00822250.
XX
PR   22-SEP-1997;   97US-00935377.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Zauderer M;
XX
DR   WPI; 2002-239252/29.
XX
PT   Representational Difference Analysis method for identification of
PT   antigens recognized by cytotoxic T cells and specific for human tumors,
PT   comprises improved selection of genes encoding target antigens.
XX
PS   Example 4; Page 19; 54pp; English.
XX
CC   The present invention relates to novel methods for the identification of
CC   antigens recognised by cytotoxic T cells (CTLs) and specific for human
CC   tumours, cancers and infected cells. The method involves screening the
CC   products of an expression library generated from DNA/RNA of a cell
CC   expressing a target epitope with cytotoxic T cells generated against the
CC   cell to identify DNA clones expressing target epitope or providing
CC   cytotoxic T cells specific for a gene product differentially expressed by
CC   a cell and measuring the cross-reactivity of the cytotoxic T cells for
CC   cells expressing a target epitope in which the target epitope is
CC   identified as a gene product inducing cytotoxic T cells. The method is
CC   useful for identifying a target epitope or antigen specific for a tumour
CC   cell. The target epitope is also useful for identifying target antigens
CC   in other target cells against which it is desirable to induce cell-
CC   mediated immunity. The antigen identified by the method is useful in
CC   immunogenic compositions and vaccine preparations to induce the
CC   regression of tumours, cancers and infections in mammals. The invention
CC   also relates to vaccinia viral vectors which are useful for treating
CC   tumour-bearing mammals, including humans to generate immune response
CC   against the tumour cells. They are also useful for immunising or
CC   vaccinating tumour-free subjects to prevent tumour formation. The present
CC   DNA sequence is an arbitrary primer which is used for modified
CC   differential display of genes encoding potential tumour immunogens. This
CC   primer is used in the exemplification of the invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
              |||||||||
Db          2 CAGACTTCA 10


RESULT 66
ABQ87208/c
ID   ABQ87208 standard; cDNA; 11 BP.
XX
AC   ABQ87208;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 963.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 77; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACT 1498
              |||||||||
Db         11 AGCCAGACT 3


RESULT 67
ABV69313/c
ID   ABV69313 standard; cDNA; 11 BP.
XX
AC   ABV69313;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7099.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
```

PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 223; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1500 CAGCAGCCA 1508
||||||||| |
Db 10 CAGCAGCCA 2

RESULT 68
ABV71907/c
ID ABV71907 standard; cDNA; 11 BP.
XX
AC ABV71907;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9693.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 313; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1490 AGCCAGACT 1498
||||||||| |
Db 11 AGCCAGACT 3

RESULT 69
ABV64486/c
ID ABV64486 standard; cDNA; 11 BP.
XX
AC ABV64486;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2272.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 88; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

```
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACT 1498
              |||||||||
Db         11 AGCCAGACT 3


RESULT 70
ABV66240
ID   ABV66240 standard; cDNA; 11 BP.
XX
AC   ABV66240;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4026.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 136; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGC 1506
              |||||||||
Db          1 TTCAGCAGC 9


RESULT 71
ABV67707/c
ID   ABV67707 standard; cDNA; 11 BP.
XX
AC   ABV67707;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5493.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 176; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         11 CAGCAGCCA 3


RESULT 72
AAQ57385/c
ID   AAQ57385 standard; mRNA; 12 BP.
XX
AC   AAQ57385;
XX
DT   25-MAR-2003  (revised)
DT   26-JUL-1994  (first entry)
XX
DE   Enzymatic RNA molecule ACE mRNA target sequence.
```

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XX
KW   Specific; cleavage; target RNA; protein; prophylaxis; expression;
KW   inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis;
KW   asthma; inflammatory diseases; cardiovascular condition; hypertension;
KW   arthritis; restenosis; angiotensin converting enzyme; ss.
XX
OS   Synthetic.
XX
PN   WO9402595-A1.
XX
PD   03-FEB-1994.
XX
PF   02-JUL-1993;   93WO-US006316.
XX
PR   17-JUL-1992;   92US-00916763.
PR   07-DEC-1992;   92US-00987132.
PR   07-DEC-1992;   92US-00989848.
PR   07-DEC-1992;   92US-00989849.
PR   19-JAN-1993;   93US-00008895.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Sullivan SM,  Draper KG;
XX
DR   WPI; 1994-048853/06.
XX
PT   Enzymatic RNA molecules which cleave mRNA - used to treat or prevent
PT   inflammatory, arthritic, stenotic or cardiovascular diseases or
PT   conditions.
XX
PS   Claim 3; Page 23; 65pp; English.
XX
CC   This is a ACE mRNA target sequence (nucleotide no. 2076) of an enzymatic
CC   RNA molecule (ribozyme) which cleaves mRNA associated with the
CC   development or maintenance of a cardiovascular condition. The concn. of
CC   the ribozyme necessary to effect a therapeutic treatment is lower than
CC   that of an antisense oligonucleotide and the specificity of action is
CC   higher. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
              |||||||||
Db         11 CAGCAGCCA 3


RESULT 73
ABI55792
ID   ABI55792 standard; DNA; 12 BP.
XX
AC   ABI55792;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 355765 for detecting SNP TSC0049803.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 355765; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAA 1487
              |||||||||
Db          1 CACGACCAA 9


RESULT 74
ABH93993
ID   ABH93993 standard; DNA; 12 BP.
XX
AC   ABH93993;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 293986 for detecting SNP TSC0015906.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 293986; 29pp + Sequence Listing; German.
XX
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```
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 7 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAA 1487
              |||||||||
Db          1 CACGACCAA 9


RESULT 75
ABH84166/c
ID   ABH84166 standard; DNA; 12 BP.
XX
AC   ABH84166;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 284159 for detecting SNP TSC0011692.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 284159; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAA 1487
              |||||||||
Db          12 CACGACCAA 4


RESULT 76
ABI32013/c
ID   ABI32013 standard; DNA; 12 BP.
XX
AC   ABI32013;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 331986 for detecting SNP TSC0036632.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 331986; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAA 1487
              |||||||||
Db          9 CACGACCAA 1


RESULT 77
ABI77576
```

ID ABI77576 standard; DNA; 12 BP.
XX
AC ABI77576;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 377549 for detecting SNP TSC0062385.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 377549; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CACGACCAA 1487
||||||||| |
Db 1 CACGACCAA 9

RESULT 78
AAQ99836
ID AAQ99836 standard; cDNA; 10 BP.
XX
AC AAQ99836;
XX
DT 06-MAR-1996 (first entry)
XX
DE Eucalyptus wood volume marker half-sib primer V7.
XX
KW Eucalyptus; urophylla; grandis; wood volume marker; RAPD genetic marker;
KW random amplified polymorphic DNA analysis; woody perennial plant;
KW family selection; pedigree; mapping; primer; ss.
XX
OS Synthetic.
XX
PN WO9519697-A1.
XX
PD 27-JUL-1995.
XX
PF 19-JAN-1995; 95WO-US000677.
XX
PR 21-JAN-1994; 94US-00184567.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Omalley DM, Sederoff RR, Grattapaglia D;
XX
DR WPI; 1995-269212/35.
XX
PT Determn. of heritable oligogenic traits in woody plants by genomic
PT mapping of multiple markers in a two generation plant family - used to
PT select plants with desired characteristics for breeding.
XX
PS Example 6; Page 58; 103pp; English.
XX
CC RAPD analysis was used to determine whether certain quantitative traits
CC were heritable oligogenic traits in Eucalyptus trees. Sets of
CC commercially available random 10-mer primers were used to amplify
CC fragments from the genomic DNA of E.urophylla, E.grandis and F1 progeny
CC obtained by crossing the two species. Subsequent mapping analysis showed
CC that the half-sib primers in AAQ99834-Q99840 are all useful for
CC amplifying wood volume markers from Eucalyptus
XX
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1488 GAAGCCAGAC 1497
|||||||| |
Db 1 GAAGCCAGCC 10

RESULT 79
AAV50097
ID AAV50097 standard; DNA; 10 BP.
XX
AC AAV50097;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for putative coding sequence locus YBR162C.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
PD 30-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001216.
XX
PR 23-JAN-1997; 97US-0035917P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-427943/36.
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle

```
PT   progression.
XX
PS   Claim 11; Page 22; 44pp; English.
XX
CC   Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC   involved in cell cycle progression selected from the group of
CC   nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC   tags for highly expressed genes and NORF genes are given in AAV50051 to
CC   AAV50345. The present invention describes: (1) a method of using yeast
CC   genes to modulate the cell cycle which comprises administering to a cell
CC   an isolated DNA molecule comprising a yeast gene which is involved in
CC   cell cycle progression selected from differentially expressed genes (SAGE
CC   tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC   antifungal drugs which comprises contacting a test substance with a yeast
CC   cell and monitoring expression of a yeast gene which is involved in cell
CC   cycle progression; (3) a method of identifying human genes which are
CC   involved in cell cycle progression which comprises hybridizing a probe
CC   comprising at least 10 contiguous nucleotides of a yeast gene which is
CC   differentially expressed between at least 2 phases selected from the log
CC   phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC   the phase in the cell cycle, where the probe comprises at least 14
CC   contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC   AAV50345), or as an array of probes on a solid support
XX
SQ   Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGA 1489
                 ||| ||||||
Db          1 ACGGCCAAGA 10


RESULT 80
AAX59809
ID   AAX59809 standard; DNA; 10 BP.
XX
AC   AAX59809;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Primer V7 for amplifying volume markers in plant half-siblings.
XX
KW   Genetic marker; genetic locus; resistance; fusiform rust disease;
KW   tree family; Pinus; volume marker; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5908978-A.
XX
PD   01-JUN-1999.
XX
PF   18-OCT-1995;   95US-00545253.
XX
PR   21-JAN-1994;   94US-00184567.
XX
PA   (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI   Grattapaglia D,  O'malley DM,  Amerson HV,  Sederoff RR,  Wilcox P;
PI   Kuhlman EG;
XX
DR   WPI; 1999-347038/29.
XX
PT   Identifying resistance to fusiform rust disease in trees of the genus
PT   Pinus.
XX
PS   Example 6; Col 37; 69pp; English.
XX
CC   The specification describes a method of identifying a genetic marker
CC   associated with a genetic locus conferring resistance to fusiform rust
CC   disease in a family of trees of the genus Pinus. The method comprises
CC   obtaining a sexually mature Pinus parent tree exhibiting resistance to
CC   fusiform rust disease, obtaining a plurality of progeny trees of the
CC   parent by self or cross-pollinations, assessing multiple progeny trees
CC   for a number of genetic markers, identifying genetic markers segregating
CC   in a Mendelian ratio and showing linkage with other genetic markers,
CC   measuring resistance to fusiform rust disease in multiple progeny trees
CC   and correlating the presence of resistance to fusiform rust disease with
CC   at least one marker identified in the previous step. The method is useful
CC   for determining the genetic basis of resistance to fusiform rust disease
CC   and for producing trees of the Pinus genus that are resistant to the
CC   disease. The present primer was to amplify volume markers in plant half-
CC   siblings, in the course of invention
XX
SQ   Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                 |||||||| |
Db          1 GAAGCCAGCC 10


RESULT 81
AAZ22666
ID   AAZ22666 standard; DNA; 10 BP.
XX
AC   AAZ22666;
XX
DT   04-JAN-2000  (first entry)
XX
DE   T18 primer for amplification of fungal genomic DNA.
XX
KW   commercial; assay; test; fungal pathogen; crop protection; cucurbit;
KW   primer; PCR; RAPD analysis; isolate; food crop; ss.
XX
OS   Synthetic.
XX
PN   EP950719-A2.
XX
PD   20-OCT-1999.
XX
PF   10-MAR-1999;   99EP-00104751.
XX
PR   16-MAR-1998;   98US-0078103P.
PR   22-FEB-1999;   99US-00255432.
XX
PA   (UYCL-) UNIV CLEMSON.
XX
PI   Keinath AP,  Somai BM,  Dean RA;
XX
DR   WPI; 1999-582557/50.
XX
PT   Detecting a pathogenic fungus in cucumbers, pumpkins and gourds using
PT   recombinant techniques.
XX
PS   Example 3; Page 8; 19pp; English.
XX
CC   This is a commercial oligonucleotide primer for the PCR-based RAPD
CC   analysis of fungal isolates of Dydimella bryiniae and Phoma species. The
CC   new method may be used to distinguish D. bryoniae from non-pathogenic
CC   Phoma species fungal infections in Cucurbits (i.e.cucumbers, pumpkins,
CC   watermelons, gourds, cantaloupes, squashes and related plants). The new
CC   method of detection of D. bryoniae and Phoma species infections allows
CC   rapid diagnosis even before symptoms are visible as compared to prior art
CC   methods which involved growing pure cultures of the pathogens from the
CC   infected plants and identifying them under the light microscope. The
CC   method leads to the early treatment of the infected plants with
CC   fungicides resulting in an increased chance of saving the infected food
CC   crops
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
```

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              || |||||||
Db          1 GATGCCAGAC 10


RESULT 82
AAZ79223
ID   AAZ79223 standard; DNA; 10 BP.
XX
AC   AAZ79223;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1651.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 112; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              ||||||| |
Db          1 GAAGCCAGCC 10


RESULT 83
AAZ82715
ID   AAZ82715 standard; DNA; 10 BP.
XX
AC   AAZ82715;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1949.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
```

```
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 111; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1499 TCAGCAGCCA 1508
              ||| ||||||
Db          1 TCAACAGCCA 10


RESULT 84
AAZ81205/c
ID   AAZ81205 standard; DNA; 10 BP.
XX
AC   AAZ81205;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #439.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 70; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||||| |||
Db         10 AAGAAGGCAG 1


RESULT 85
AAZ82619
ID   AAZ82619 standard; DNA; 10 BP.
XX
AC   AAZ82619;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1853.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
```

PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 108; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1488 GAAGCCAGAC 1497
||||||||| |
Db 1 GAAGCCAGCC 10

RESULT 86
AAZ84503
ID AAZ84503 standard; DNA; 10 BP.
XX
AC AAZ84503;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3737.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 158; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1486 AAGAAGCCAG 1495
||||||| ||
Db 1 AAGAAGCAAG 10

RESULT 87
AAZ84255
ID AAZ84255 standard; DNA; 10 BP.
XX
AC AAZ84255;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3489.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX

```
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 152; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              |||||| |||
Db          1 AGAAGCAAGA 10


RESULT 88
AAZ81942/c
ID   AAZ81942 standard; DNA; 10 BP.
XX
AC   AAZ81942;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1176.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 90; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              ||| ||||||
Db         10 CCAGGAAGCC 1


RESULT 89
AAA11232
ID   AAA11232 standard; DNA; 10 BP.
XX
AC   AAA11232;
XX
DT   25-OCT-2000  (first entry)
XX
DE   RAPD primer U-12 for detecting Leishmania species.
XX
KW   Identification; Leishmania; isoenzyme; amplicon; promastigote; diagnosis;
KW   PCR primer; amplification; epidemiology; vaccine; ss.
XX
OS   Leishmania sp.
```

XX
PN FR2786202-A1.
XX
PD 26-MAY-2000.
XX
PF 19-NOV-1998; 98FR-00014567.
XX
PR 19-NOV-1998; 98FR-00014567.
XX
PA (FRRE-) INST FR RECH SCI DEV EN COOP ORSTOM.
XX
DR WPI; 2000-389570/34.
XX
PT Identifying species of Leishmania, useful e.g. for diagnosis and
PT selection of treatment, using a limited set of isoenzymes or
PT amplification primers for differentiation.
XX
PS Claim 2; Page 26; 30pp; French.
XX
CC The invention relates to a method for identifying Leishmania species by
CC identifying isoenzymes and/or amplicons from, respectively, proteins or
CC DNA extracted from cultured promastigotes derived from an isolate. The
CC method uses a limited set of isoenzymes and/or amplification primers that
CC are discriminatory for characteristics of a broad spectrum of Leishmania
CC species. The isoenzymes used for detection include Glucose Phosphate
CC Isomerase (GPI), Mannose Phosphate Isomerase (MPI), Nucleoside Hydrolase
CC substrate deoxyinosine (NHD) and Phosphoglucomutase (PGM). The
CC amplification primers used for PCR identification include primers
CC AAA11223-A11232. The method is used to identify specific Leishmania
CC species, either for diagnosis or for selection of appropriate treatments,
CC also in epidemiological studies and for preparation of pharmaceuticals
CC and vaccines
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1499 TCAGCAGCCA 1508
||| ||||||
Db 1 TCACCAGCCA 10

RESULT 90
AAH63301/c
ID AAH63301 standard; cDNA; 10 BP.
XX
AC AAH63301;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 141.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 1; Page 42; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1496 ACTTCAGCAG 1505
|||| |||||
Db 10 ACTTAAGCAG 1

RESULT 91
AAH63452
ID AAH63452 standard; cDNA; 10 BP.
XX
AC AAH63452;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 292.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 45; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;

```
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1499 TCAGCAGCCA 1508
              ||| ||||||
Db          1 TCAACAGCCA 10


RESULT 92
AAH64237/c
ID   AAH64237 standard; cDNA; 10 BP.
XX
AC   AAH64237;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1077.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 63; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTT 1499
              |||||| |||
Db         10 AGCCAGTCTT 1


RESULT 93
ABA06059/c
ID   ABA06059 standard; cDNA; 10 BP.
XX
AC   ABA06059;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 36.
XX
KW   Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001211883-A.
XX
PD   07-AUG-2001.
XX
PF   31-JAN-2000; 2000JP-00023170.
XX
PR   31-JAN-2000; 2000JP-00023170.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-629566/73.
XX
PT   Human normal hepatccyte expression gene group.
XX
PS   Claim 1; Page 6; 26pp; Japanese.
XX
CC   The invention relates to a human normal hepatocyte expression gene group
CC   comprising 200 genes in the human normal hepatocyte. The cDNA of each
CC   gene comprises one of 200 fully defined nucleotide sequences as given in
CC   the specification. The gene group and the cDNAs corresponding to each of
CC   the genes in the group are useful in the diagnosis and treatment of human
CC   hepatopathy. The present sequence is a cDNA corresponding to a gene
CC   expressed by normal human hepatocytes
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              | ||||||||
Db         10 AGGCCAGACT 1


RESULT 94
AAF38816
ID   AAF38816 standard; DNA; 10 BP.
XX
AC   AAF38816;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5555.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
```

XX
PS Example; Page 198; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1486 AAGAAGCCAG 1495
|||||| |||
Db 1 AAGAAGACAG 10

RESULT 95
AAF39726
ID AAF39726 standard; DNA; 10 BP.
XX
AC AAF39726;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6465.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 230; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1487 AGAAGCCAGA 1496
|| |||||||
Db 1 AGGAGCCAGA 10

RESULT 96
AAF40474
ID AAF40474 standard; DNA; 10 BP.
XX
AC AAF40474;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7213.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;

```
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 257; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCA 1494
              ||| ||||||
Db          1 CAACAAGCCA 10


RESULT 97
AAF40855
ID   AAF40855 standard; DNA; 10 BP.
XX
AC   AAF40855;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7594.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 271; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1492 CCAGACTTCA 1501
              ||||| ||||
Db          1 CCAGAGTTCA 10


RESULT 98
AAF35202
ID   AAF35202 standard; DNA; 10 BP.
XX
AC   AAF35202;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1941.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
```

XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 69; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGA 1489
              | ||||||||
Db          1 AAGACCAAGA 10
```

RESULT 99
AAF36577/c
ID AAF36577 standard; DNA; 10 BP.
XX
AC AAF36577;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3316.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX

PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 118; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              ||| ||||||
Db         10 CTTGAGCAGC 1
```

RESULT 100
AAF36581/c
ID AAF36581 standard; DNA; 10 BP.
XX
AC AAF36581;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3320.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.

```
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 118; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 ACCAAGAAGC 1492
              ||||| ||||
Db         10 ACCAAAAAGC 1


RESULT 101
AAF38900
ID   AAF38900 standard; DNA; 10 BP.
XX
AC   AAF38900;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5639.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 201; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              ||| ||||||
Db          1 AAGGAGCCAG 10


RESULT 102
AAF33314
ID   AAF33314 standard; DNA; 10 BP.
XX
AC   AAF33314;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast putative coding sequence SAGE tag oligonucleotide SEQ ID NO:53.
XX
```

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 22; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGA 1489
              ||| ||||||
Db          1 ACGGCCAAGA 10
```

RESULT 103
AAF34250
ID AAF34250 standard; DNA; 10 BP.
XX
AC AAF34250;
XX
DT 23-MAR-2001 (first entry)

XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:989.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 35; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1480 ACGACCAAGA 1489
              ||| ||||||
Db          1 ACGGCCAAGA 10
```

RESULT 104
AAF35602/c
ID AAF35602 standard; DNA; 10 BP.
XX

```
AC   AAF35602;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2341.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 83; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              |||||| |||
Db         10 CTTCAGGAGC 1


RESULT 105
AAF38822
ID   AAF38822 standard; DNA; 10 BP.
XX
AC   AAF38822;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5561.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 198; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||||||| |
Db          1 AAGAAGCCGG 10
```

```
RESULT 106
AAF41495/c
ID   AAF41495 standard; DNA; 10 BP.
XX
AC   AAF41495;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8234.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V;  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 294; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match           28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              ||| ||||||
Db         10 AAGGAGCCAG 1

RESULT 107
AAF34426
ID   AAF34426 standard; DNA; 10 BP.
XX
AC   AAF34426;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1165.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 41; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match           28.0%;  Score 8.4;  DB 1;  Length 10;
```

```
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCA 1494
              |||||||| |
Db          1 CAAGAAGCTA 10


RESULT 108
AAF34234/c
ID   AAF34234 standard; DNA; 10 BP.
XX
AC   AAF34234;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:973.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 34; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCA 1504
              ||||||| ||
Db          10 GACTTCACCA 1


RESULT 109
AAS19669
ID   AAS19669 standard; DNA; 10 BP.
XX
AC   AAS19669;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Primer-extension oligonucleotide #22 to detect human GHRHR polymorphisms.
XX
KW   Human; single nucleotide polymorphism; SNP; GHRHR; chromosome 7p14;
KW   growth hormone releasing hormone receptor; haplotyping; genotyping;
KW   isolated growth hormone deficiency; IGHD; pituitary adenoma; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179239-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US012453.
XX
PR   17-APR-2000; 2000US-0197978P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Denton RR,  Nandabalan K,  Sausker EA;
XX
DR   WPI; 2002-066342/09.
XX
PT   Genotyping human Growth hormone releasing hormone receptor gene of
PT   individual for determining haplotype of individual by determining
PT   identity of nucleotide pair at specific polymorphic sites for two copies
PT   of gene.
XX
PS   Claim 18; Page 15; 90pp; English.
XX
CC   The present invention relates to novel single nucleotide polymorphisms
CC   (SNPs) in the human growth hormone releasing hormone receptor (GHRHR)
CC   gene located on chromosome 7p14, and methods for haplotyping and/or
CC   genotyping the GHRHR gene. The methods of the invention make use of
CC   allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC   primer-extension oligonucleotides for detecting the GHRHR gene
CC   polymorphisms. The polynucleotides and screened compounds are useful for
CC   the treatment of diseases associated with GHRHR activity, such as
CC   isolated growth hormone deficiency (IGHD) and pituitary adenomas.
CC   AAS19648-AAS19673 represent primer-extension oligonucleotides for
CC   detecting human GHRHR gene polymorphisms
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              |||||| |||
Db          1 GAAGCCTGAC 10


RESULT 110
ABL52200
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```
ID   ABL52200 standard; DNA; 10 BP.
XX
AC   ABL52200;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 preferred oligonucleotide primer SEQ ID NO:125.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US028780.
XX
PR   13-SEP-2000; 2000US-0232468P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of the
PT   polynucleotide, and for expressing the homolog.
XX
PS   Claim 19; Page 16; 162pp; English.
XX
CC   The present invention describes an isolated human period (Drosophila)
CC   homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC   polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC   or its fragment, or a polymorphic variant of a reference sequence
CC   (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC   describes methods for genotyping and haplotyping the PER1 gene of an
CC   individual. (I) is useful in studying the expression and function of
CC   PER1, and in expressing PER1 protein for use in screening for candidate
CC   drugs to treat diseases related to PER1 activity. (I) is useful for
CC   therapeutic purposes. A recombinant non-human organism transformed or
CC   transfected with (I) can be used for studying expression of the PER1
CC   isogenes in vivo, for in vivo screening and testing of drugs targeted
CC   against PER1 protein, and for testing the efficacy of therapeutic agents
CC   and compounds for disorders associated with circadian rhythm regulation.
CC   The present sequence represents a preferred oligonucleotide primer for
CC   human PER1, which is used in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              | ||||||||
Db          1 CGTCAGCAGC 10


RESULT 111
ABK81399/c
ID   ABK81399 standard; DNA; 10 BP.
XX
AC   ABK81399;
XX
DT   13-AUG-2002  (first entry)
XX
DE   SCYA21 gene primer extension oligonucleotide #3.
XX
KW   Small inducible cytokine subfamily A (Cys-Cys) member 21; SCYA21;
KW   polymorphism; haplotype; immunological disorder; gene expression;
KW   drug development; immunomodulator; primer extension; oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200232930-A2.
XX
PD   25-APR-2002.
XX
PF   09-OCT-2001; 2001WO-US046141.
XX
PR   19-OCT-2000; 2000US-0241622P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Russo DP;
XX
DR   WPI; 2002-435528/46.
XX
PT   New genetic variants comprising haplotypes of the small inducible
PT   cytokine subfamily A, member 21 (SCYA21) gene, useful in improving the
PT   efficiency of screening for drugs for treating immunological disorders or
PT   for targeting SCYA21.
XX
PS   Claim 16; Page 13; 56pp; English.
XX
CC   The invention describes an isolated polynucleotide, which comprises genes
CC   and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),
CC   member 21 (SCYA21) gene. The polynucleotide comprises polymorphic sites
CC   referred to as PS1-5 to designate the order in which they are located in
CC   the gene. The polymorphisms and haplotypes of SCYA21 gene are useful for
CC   validating whether SCYA21 is a suitable target for drugs to treat
CC   immunological disorders and disorders associated with its abnormal
CC   expression or function, screening for such drugs and reducing bias in
CC   clinical trials of such drugs. Haplotype information would be useful in
CC   improving the efficiency and output of several steps in the drug
CC   discovery and development process, including target validation,
CC   identifying lead compounds and early phase clinical trials. The methods
CC   are useful in screening for compounds targeting SCYA21 to treat a
CC   specific condition or disease predicted to be associated with SCYA21
CC   activity, e.g. immunological disorders. This sequence represents a primer
CC   extension oligonucleotide used to identify polymorphic sites in the
CC   SCYA21 gene
XX
SQ   Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              ||| ||||||
Db         10 AGAGGCCAGA 1


RESULT 112
ABK96063/c
ID   ABK96063 standard; DNA; 10 BP.
XX
AC   ABK96063;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human LIPE gene polymorphism detection oligonucleotide primer #38.
XX
KW   Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
KW   polymorphism; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200240502-A2.
XX
PD   23-MAY-2002.
```

XX
PF 16-NOV-2001; 2001WO-US043518.
XX
PR 16-NOV-2000; 2000US-0249302P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
XX
DR WPI; 2002-519369/55.
XX
PT Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPE activity, e.g. obesity and male sterility.
XX
PS Claim 17; Page 16; 142pp; English.
XX
CC The present invention relates to a new polynucleotide comprising a
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
CC isogenes. The invention is useful in screening for drugs targeting LIPE
CC isogenes that are useful for treating obesity and male sterility. The
CC methods of the invention are useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with LIPE activity. The polynucleotide
CC is useful in studying the expression and function of LIPE, and in
CC expressing LIPE protein for use in screening for candidate drugs to treat
CC diseases related to LIPE activity. It is also useful in studying the
CC effect of the variation on the biological activity of LIPE as well as on
CC the binding affinity of candidate drugs targeting LIPE for the treatment
CC of obesity and male sterility. The invention is useful for studying the
CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against LIPE protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating obesity and male sterility
CC in a biological system. The present nucleic acid sequence represents one
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
CC used in the invention to detect polymorphisms in the human LIPE gene
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1494 AGACTTCAGC 1503
              ||||||| ||
Db         10 AGACTTCCGC 1
```

RESULT 113
AAD25204
ID AAD25204 standard; DNA; 10 BP.
XX
AC AAD25204;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human homeo box D3 (HOXD3) gene polymorphism detecting primer #3.
XX
KW Human; homeo box D3; HOXD3; polymorphism; developmental disorder;
KW haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy;
KW drug screening; cytostatic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190127-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US016982.
XX
PR 25-MAY-2000; 2000US-0207076P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kazemi A, Koshy B, Kumar AM;
XX
DR WPI; 2002-075363/10.
XX
PT New genetic variants of Homeo Box D3 for studying expression and function
PT of the protein, and for screening drugs to treat diseases e.g.
PT developmental disorders and tumors.
XX
PS Claim 18; Page 13; 66pp; English.
XX
CC The invention relates to genetic variants of the homeo box D3 (HOXD3)
CC gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes (HTS)
CC or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC HOXD3 activity, e.g., developmental disorders and tumours. HOXD3 isogene
CC is useful in studying the expression and function of HOXD3 and in
CC expressing HOXD3 protein for use in screening for candidate drugs to
CC treat diseases related to HOXD3 activity and in studying the effect of
CC the variation on the biological activity of HOXD3 as well as on the
CC binding affinity of candidate drugs targeting HOXD3 for the treatment of
CC developmental disorders and tumours. An antibody against HOXD3 is useful
CC in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A recombinant non-human organism is useful in studying
CC expression of the HOXD3 isogenes in vivo. Allele-specific
CC oligonucleotides (ASO) are useful as probes and primers and for assaying
CC a polymorphism in the target region. The present sequence is a primer
CC used for detecting human HOXD3 gene polymorphisms
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1499 TCAGCAGCCA 1508
              ||||||| ||
Db          1 TCAGCAGACA 10
```

RESULT 114
ABV84823/c
ID ABV84823 standard; cDNA; 10 BP.
XX
AC ABV84823;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human haemopexin SAGE tag #633.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-00012328.
XX
PR 19-JAN-2001; 2001JP-00012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
XX
PS Claim 55; Page 28; 139pp; Japanese.

```
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
CC   expressed in chronic hepatitis C liver tissue
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              | ||||||||
Db         10 AGGCCAGACT 1


RESULT 115
ABK54423/c
ID   ABK54423 standard; DNA; 10 BP.
XX
AC   ABK54423;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human ISL1 gene ASO primer extension sequence #18.
XX
KW   Human; ss; primer; ISL1; islet-1; chromosome 5q; motor neuron defect;
KW   diabetes; transcription factor; LIM; homeodomain; antidiabetic; PCR;
KW   gene therapy; primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200212498-A2.
XX
PD   14-FEB-2002.
XX
PF   06-AUG-2001; 2001WO-US024664.
XX
PR   04-AUG-2000; 2000US-0223535P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kliem SE,  Koshy B,  Tanguay DA;
XX
DR   WPI; 2002-280693/32.
XX
PT   Novel isolated polynucleotide which is a polymorphic variant of ISL1
PT   transcription factor, LIM/Homeodomain, (islet-1) (ISL1) used for
PT   expressing ISL1 protein isoform and for screening drug candidates to
PT   treat diabetes.
XX
PS   Claim 18; Page 14; 90pp; English.
XX
CC   The invention relates to an isolated polynucleotide sequence which
CC   comprises ISL1 transcription factor (islet-1, of the LIM/Homeodomain
CC   family), isogene and the polymorphic variants of the coding region
CC   (cDNA). Also included are a recombinant non-human organism expressing
CC   ISL1, haplotyping/genotyping an individual by determining which
CC   polymorphism is present in one or both copies of the ISL1 gene, for one
CC   or more polymorphic sites, identifying an association between a trait and
CC   a haplotype pair, an isolated oligonucleotide for detecting a
CC   polymorphism in the ISL1 gene, polymorphic variant of the ISL1 protein,
CC   an anti-ISL1 monoclonal antibody and a computer system for storing and
CC   analysing polymorphism data. The ISL1 polymorphic variant polypeptide is
CC   useful for screening drugs which involves contacting it with a candidate
CC   agent and assaying for binding activity. The polymorphic variant is
CC   useful for studying expression and function of ISL1 and expressing ISL1
CC   protein for use in screening for candidate drugs to treat diseases
CC   related to ISL1 activity (e.g. diabetes and motor neuron defects). The
CC   polymorphism and haplotype data is useful for validating whether ISL1 is
CC   a suitable target for drugs to treat disorders related to defects in
CC   motor neuron and diabetes, screening for such drugs and reducing bias in
CC   clinical trials of such drugs. The polymorphic variant is also useful for
CC   therapeutic purposes. The method is also useful for screening compounds
CC   to treat a specific condition or disease predicted to be associated with
CC   ISL1 activity. The ISL1 gene is located on human chromosome 5q. The
CC   present sequence is the 3' terminus of an allele specific oligonucleotide
CC   (ASO) primer extension primer used to detect the ISL1 polymorphisms
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCA 1504
              | ||||||||
Db         10 GGCTTCAGCA 1


RESULT 116
ABK11491
ID   ABK11491 standard; DNA; 10 BP.
XX
AC   ABK11491;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Oligonucleotide primer #3, to detect human ADRB3 gene polymorphisms.
XX
KW   Human; beta-3-adrenergic; receptor; ADRB3; primer; anorectic; ss;
KW   antidiabetic; gene therapy; morbid obesity; insulin resistance;
KW   non-insulin-dependent diabetes mellitus; haplotyping; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200208425-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-US023223.
XX
PR   21-JUL-2000; 2000US-0220088P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Finkel K,  Koshy B;
XX
DR   WPI; 2002-241571/29.
XX
PT   Novel genetic variants of beta-3-adrenergic receptor gene useful in
PT   studying expression and function of the protein, and for screening drugs
PT   to treat diseases e.g. obesity, non-insulin dependent diabetes mellitus.
XX
PS   Claim 19; Page 15; 91pp; English.
XX
CC   The present invention relates to a new polypeptide comprising a sequence
CC   which is a polymorphic variant of a reference sequence for ADRB3 (beta-3-
CC   adrenergic receptor) protein. The reference sequence comprises a sequence
```

CC of 408 amino acids as given in the specification, or its fragment, and
CC the polymorphic variant comprises one or more variant amino acids. The
CC polymorphic variants are useful in studying the expression and function
CC of ADRB3, in expressing ADRB3 protein for use in screening for candidate
CC drugs to treat diseases related to ADRB3 activity, in studying the effect
CC of the variation on the biological activity of ADRB3, and the binding
CC affinity of candidate drugs targeting ADRB3 for the treatment of
CC disorders such as morbid obesity, insulin resistance and an early onset
CC of non-insulin-dependent diabetes mellitus. Haplotyping methods are
CC useful in validating ADRB3 as a candidate target for treating a specific
CC condition or disease predicted to be associated with ADRB3 activity, or
CC in the design of clinical trials of candidate drugs for treating a
CC specific condition or disease associated with ADRB3 activity. The present
CC nucleic acid sequence represents one of a collection of oligonucleotide
CC primers (ABK11489- ABK11512) that were used in the methods of the
CC invention to detect polymorphisms in the human ADRB3 gene
XX
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCC 1493
||| ||||||
Db 1 CCAGGAAGCC 10

RESULT 117
ABK72629
ID ABK72629 standard; DNA; 10 BP.
XX
AC ABK72629;
XX
DT 30-JUL-2002 (first entry)
XX
DE Leukotriene B4 receptor primer extension oligonucleotide #1.
XX
KW Human; leukotriene B4; receptor; chemokine receptor-like 1; LTB4R;
KW chemoattractant; inflammation; immune response; infection;
KW inflammatory disorder; recombinant non-human animal;
KW primer extension oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200230949-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032002.
XX
PR 13-OCT-2000; 2000US-0240223P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Chew A, Koshy B, Sanchis A, Sausker EA;
XX
DR WPI; 2002-416857/44.
XX
PT Novel isolated human leukotriene B4 receptor polynucleotide, useful for
PT therapeutic purposes, for studying expression and function of the
PT polynucleotide, and for expressing the receptor.
XX
PS Claim 17; Page 14; 69pp; English.
XX
CC The invention describes an isolated human leukotriene B4 receptor
CC (chemokine receptor-like 1) (LTB4R) polynucleotide (I) comprising a
CC sequence which is a polymorphic variant for a reference sequence for the
CC LTB4R gene or its fragment, or a polymorphic variant of a reference
CC sequence for a LTB4R cDNA or its fragment. LTB4R is a potent
CC chemoattractant that is primarily involved in inflammation, immune
CC responses and host defense against infection. (I) is useful in studying
CC the expression and function of LTB4R, and in expressing LTB4R protein for
CC use in screening for candidate drugs to treat diseases related to LTB4R
CC activity, e.g. inflammatory disorders. A recombinant non-human animal is
CC useful for studying expression of the LTB4R isogenes in vivo, for in vivo
CC screening and testing of drugs targeted against LTB4R protein, and for
CC testing the efficacy of therapeutic agents and compounds for diseases
CC associated with LTB4R activity, e.g. inflammatory disorders, in a
CC biological system. This sequence represents a primer extension
CC oligonucleotide used for detecting polymorphisms in the leukotriene B4
CC receptor (LTB4R) gene
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGC 1506
|||| |||||
Db 1 CTTCTGCAGC 10

RESULT 118
ACA94480/c
ID ACA94480 standard; DNA; 10 BP.
XX
AC ACA94480;
XX
DT 18-JUL-2003 (first entry)
XX
DE DNA tag from human transcript elevated in adenomas/cancers #61.
XX
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
KW kidney proximal tubule.
XX
OS Homo sapiens.
XX
PN WO2003022863-A1.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028518.
XX
PR 07-SEP-2001; 2001US-0317494P.
PR 30-MAY-2002; 2002US-0383805P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Buckhaults P, Kinzler KW, Vogelstein B;
XX
DR WPI; 2003-313220/30.
XX
PT Detecting colorectal cancer in a subject, involves detecting macrophage
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
PT of the subject.
XX
PS Disclosure; Page 26; 59pp; English.
XX
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
CC amount of MIC or RDP detected to that in normal subjects, where an
CC elevated amount of MIC or RDP in the subject is an indicator of CC in
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
CC mRNA detected to that in normal subjects, where an elevated amount of MIC
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
CC isolating epithelial cells from blood of a subject, isolating an mRNA
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
CC of CC in the subject; (d) contacting blood or faeces of a subject, with

```
CC   an RDP substrate, detecting activity of RDP in the blood or faeces by
CC   detection of increased reaction product or decreased RDP substrate, and
CC   comparing the amount of activity of RDP in blood or faeces of the subject
CC   to that in normal subjects, where an elevated amount of activity of RDP
CC   in the blood or faeces of the subject is an indicator of CC in the
CC   subject; (e) administering to a subject an antibody which specifically
CC   binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
CC   labeled with a moiety which is detectable from outside of the subject and
CC   detecting the moiety in the subject from outside of the subject, where an
CC   area of localisation of the moiety within the subject but outside the
CC   proximal tubules of the kidney identifies CC; or (f) administering to a
CC   subject a substrate for RDP, the substrate being labeled with a
CC   detectable moiety, isolating faeces or blood from the subject, and
CC   detecting in the faeces or blood RDP reaction product or RDP substrate
CC   with the detectable moiety, where increased product or decreased
CC   substrate in the faeces or blood indicates CC in the subject. The methods
CC   are useful for detecting colorectal cancer in a subject. The present
CC   sequence is a DNA tag derived from a human transcript whose expression is
CC   elevated in colorectal cancer or colorectal adenoma
XX
SQ   Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1492 CCAGACTTCA 1501
              |||||| |||
Db         10 CCAGACATCA 1

RESULT 119
ABT14411
ID   ABT14411 standard; DNA; 10 BP.
XX
AC   ABT14411;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Nucleic acid PCR amplification method-related RAPD PCR primer #181.
XX
KW   Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW   RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS   Unidentified.
XX
PN   WO200281743-A2.
XX
PD   17-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-GB001489.
XX
PR   02-APR-2001; 2001GB-00008182.
XX
PA   (HAMI/) HAMILL B.
XX
PI   Hamill B;
XX
DR   WPI; 2003-075484/07.
XX
PT   Amplification of nucleotide sequences from polynucleotides by chain
PT   extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT   solution, 2 attached to supports and both share complementary sequences.
XX
PS   Disclosure; Fig 17; 60pp; English.
XX
CC   The invention comprises a method for the PCR amplification of nucleic
CC   acids. The method involves a set of primers, where two of the primers are
CC   in solution and at least two other primers are attached to a solid
CC   support. The method of the invention can be used for the analysis of a
CC   nucleic acid or a mixture of nucleic acids, including: single-stranded
CC   DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC   present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC   PCR primer of the invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              || |||||||
Db          1 GATGCCAGAC 10

RESULT 120
ABT14323
ID   ABT14323 standard; DNA; 10 BP.
XX
AC   ABT14323;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Nucleic acid PCR amplification method-related RAPD PCR primer #93.
XX
KW   Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW   RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS   Unidentified.
XX
PN   WO200281743-A2.
XX
PD   17-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-GB001489.
XX
PR   02-APR-2001; 2001GB-00008182.
XX
PA   (HAMI/) HAMILL B.
XX
PI   Hamill B;
XX
DR   WPI; 2003-075484/07.
XX
PT   Amplification of nucleotide sequences from polynucleotides by chain
PT   extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT   solution, 2 attached to supports and both share complementary sequences.
XX
PS   Disclosure; Fig 17; 60pp; English.
XX
CC   The invention comprises a method for the PCR amplification of nucleic
CC   acids. The method involves a set of primers, where two of the primers are
CC   in solution and at least two other primers are attached to a solid
CC   support. The method of the invention can be used for the analysis of a
CC   nucleic acid or a mixture of nucleic acids, including: single-stranded
CC   DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC   present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC   PCR primer of the invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 56;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||| |||||
Db          1 AAGAGGCCAG 10

RESULT 121
AAX14955/c
ID   AAX14955 standard; DNA; 11 BP.
XX
AC   AAX14955;
```

XX
DT 27-AUG-2003 (revised)
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of 23S rRNA gene nucleotides 486-496.
XX
KW Triplex formation; DNA detection; triple helix; identification; bacteria;
KW oncogene; virus; ss.
XX
OS Synthetic.
OS Pseudomonas sp.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 25-26; 168pp; English.
XX
CC The present sequence represents a polynucleotide that is able to form a
CC triple helix with a double stranded sequence. Cytosine bases in the
CC present can be replaced with 5-methylcytosine for increased triplex
CC stability. The present sequence is used in the assay of the invention,
CC where it can be part of the anchor DNA or reporter DNA sequence. The
CC assay comprises adding a sample containing double-stranded DNA test
CC sequences to an aqueous medium containing at least one complex of anchor
CC DNA, attached to a solid support, and reporter DNA, where either a part
CC of the anchor DNA or reporter DNA is designed to form a triple-strand
CC structure with part of the test sequence. Triplex formation results in
CC displacement of the reporter DNA which is detected as an indication of
CC the presence of the DNA test sequence. The method is used to detect DNA
CC sequences, particularly for identification of bacteria (by detecting
CC genes for ribosomal RNA) in clinical samples, but also detection of
CC oncogenes and Hepatitis B virus. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1482 GACCAAGAAG 1491
|| |||||||
Db 11 GAACAAGAAG 2

RESULT 122
ABQ86554
ID ABQ86554 standard; cDNA; 11 BP.
XX
AC ABQ86554;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 309.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 49; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCC 1493
|||||| |||
Db 2 CCAAGATGCC 11

RESULT 123
ABQ86306/c
ID ABQ86306 standard; cDNA; 11 BP.
XX
AC ABQ86306;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 61.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX

```
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 39; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              |||| |||||
Db         11 TTCACCAGCC 2


RESULT 124
ABQ87206/c
ID   ABQ87206 standard; cDNA; 11 BP.
XX
AC   ABQ87206;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 961.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 77; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1479 CACGACCAAG 1488
              |||||||| |
Db         11 CACGACCACG 2


RESULT 125
ABV64744/c
ID   ABV64744 standard; cDNA; 11 BP.
XX
AC   ABV64744;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2530.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 95; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCAG 1502
              ||| ||||||
Db         10 CAGCCTTCAG 1
```

```
RESULT 126
ABV67763
ID   ABV67763 standard; cDNA; 11 BP.
XX
AC   ABV67763;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5549.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 178; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              |||| |||||
Db          2 AGAAACCAGA 11


RESULT 127
ABV69450
ID   ABV69450 standard; cDNA; 11 BP.
XX
AC   ABV69450;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7236.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 227; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              ||| ||||||
Db          2 CCAGGAAGCC 11


RESULT 128
ABV69082/c
ID   ABV69082 standard; cDNA; 11 BP.
XX
AC   ABV69082;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6863.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
```

PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 216; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1492 CCAGACTTCA 1501
|||||| |||
Db 10 CCAGACATCA 1

RESULT 129
ABV66348/c
ID ABV66348 standard; cDNA; 11 BP.
XX
AC ABV66348;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4134.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 139; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1493 CAGACTTCAG 1502
||| ||||||
Db 11 CAGGCTTCAG 2

RESULT 130
ABV66542
ID ABV66542 standard; cDNA; 11 BP.
XX
AC ABV66542;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4328.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 144; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;

```
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTT 1499
              | ||||||||
Db          2 ACCCAGACTT 11


RESULT 131
ABV66760
ID   ABV66760 standard; cDNA; 11 BP.
XX
AC   ABV66760;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4546.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 150; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              ||||||| ||
Db          1 AAGCCAGTCT 10


RESULT 132
ABV68413/c
ID   ABV68413 standard; cDNA; 11 BP.
XX
AC   ABV68413;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6199.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 197; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              |||| |||||
Db         11 TTCACCAGCC 2


RESULT 133
ABV69080/c
ID   ABV69080 standard; cDNA; 11 BP.
XX
AC   ABV69080;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6866.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
```

PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 216; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCC 1493
||| ||||||
Db 10 CCAGGAAGCC 1

RESULT 134
ABV68371
ID ABV68371 standard; cDNA; 11 BP.
XX
AC ABV68371;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6157.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 196; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCC 1493
|||||| |||
Db 2 CCAAGATGCC 11

RESULT 135
ABV68621
ID ABV68621 standard; cDNA; 11 BP.
XX
AC ABV68621;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6407.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 203; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

```
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              || |||||||
Db          2 CTCCAGCAGC 11


RESULT 136
ABV63846/c
ID   ABV63846 standard; cDNA; 11 BP.
XX
AC   ABV63846;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1632.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 69; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              |||| |||||
Db          11 CTTCCGCAGC 2


RESULT 137
ABV65219
ID   ABV65219 standard; cDNA; 11 BP.
XX
AC   ABV65219;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3005.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 108; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              |||||| |||
Db          1 AGAAGCAAGA 10


RESULT 138
ABV66909/c
ID   ABV66909 standard; cDNA; 11 BP.
XX
AC   ABV66909;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4695.
XX
```

KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 154; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CACGACCAAG 1488
||||||||| |
Db 11 CACGACCACG 2

RESULT 139
ABV71267/c
ID ABV71267 standard; cDNA; 11 BP.
XX
AC ABV71267;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9053.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 291; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1497 CTTCAGCAGC 1506
|||| |||||
Db 11 CTTCCGCAGC 2

RESULT 140
ABV67181
ID ABV67181 standard; cDNA; 11 BP.
XX
AC ABV67181;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4967.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 162; 1345pp; German.
XX

```
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              |||||.|| |||
Db          2 CTTCAGTAGC 11


RESULT 141
ABV66102/c
ID   ABV66102 standard; cDNA; 11 BP.
XX
AC   ABV66102;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3888.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 132; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1494 AGACTTCAGC 1503
              ||||| ||||
Db         11 AGACTGCAGC 2


RESULT 142
AAS21210/c
ID   AAS21210 standard; DNA; 11 BP.
XX
AC   AAS21210;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transmissible gastroenteritis virus full length clone, C/DE-1 junction.
XX
KW   Transmissible gastroenteritis virus; TGE; gene transfer;
KW   recombinant viral genome; gene therapy; artificial chromosome; vaccine;
KW   ds.
XX
OS   Transmissible gastroenteritis virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(6,T)
FT                   /*tag=  a
FT   misc_feature    7. .8
FT                   /*tag=  b
FT                   /label= Cleavage_site
FT                   /note= "Restriction enzyme Bgl1 cleaves at this site
FT                   creating a sticky end"
FT   mutation        replace(10,A)
FT                   /*tag=  c
XX
PN   WO200190340-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US016564.
XX
PR   21-MAY-2000; 2000US-0206537P.
PR   20-APR-2001; 2001US-0285320P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Baric RS,  Yount B;
XX
DR   WPI; 2002-114288/15.
XX
PT   Directionally assembling a recombinant viral genome, useful for
PT   manipulating the genomes of plants, animals, bacteria or viruses for gene
PT   therapy, by ligating the subclones of the viral genome to assemble a
PT   recombinant viral genome.
XX
PS   Example 7; Page 22; 42pp; English.
XX
CC   The invention describes a method of directionally assembling a
CC   recombinant viral genome comprising ligating the subclones of the viral
CC   genome to assemble a recombinant viral genome, particularly coronavirus.
CC   For directionally assembling a recombinant viral genome. In particular,
CC   the method is useful for manipulating the genomes of higher plants and
CC   animals, as well as bacteria and viruses. In particular, the method is
CC   useful for the precise genetic manipulation of individual chromosomes in
CC   whole plants and animals and the construction of artificial chromosomes
CC   for gene therapy. The genomes produced are useful in preparing vaccines
CC   and expression vectors (e.g., TGE vectors and vaccines), which are useful
CC   in protocols involving vaccination, gene transfer and gene therapy. This
CC   sequence represents the interconnecting junction site C/DE-1 used in the
```

```
CC   assembly of the full length transmissible gastroenteritis virus (TGE)
CC   genome described in the method of the invention
XX
SQ   Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              |||||||| |
Db         10 CCAAGAAGGC 1


RESULT 143
ABT16435/c
ID   ABT16435 standard; DNA; 11 BP.
XX
AC   ABT16435;
XX
DT   20-MAR-2003  (first entry)
XX
DE   Human neurokinin 1 receptor gene polymorphic region SEQ ID No 16.
XX
KW   Cytostatic; antiasthmatic; antiinflammatory; cardiant; polymorphic site;
KW   human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
KW   TACR1 ligand mediated disease; asthma; paternity testing; cancer;
KW   inflammation; heart disease; central nervous system; infection; ds.
XX
OS   Homo sapiens.
XX
PN   EP1262565-A2.
XX
PD   04-DEC-2002.
XX
PF   23-MAY-2002; 2002EP-00253662.
XX
PR   25-MAY-2001; 2001US-0293425P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Affourtit JP,  Nelson DL,  Seymour AB,  Webb SM;
XX
DR   WPI; 2003-150228/15.
XX
PT   Novel nucleic acid segment from human neurokinin 1 receptor, including
PT   polymorphic sites for diagnosing and treating asthma, and in forensics,
PT   paternity testing, and genetic mapping of the traits.
XX
PS   Claim 1; Page 25; 27pp; English.
XX
CC   The invention relates to a nucleic acid segment from the human neurokinin
CC   1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
CC   having a polymorphic site or a complement of the fragment. The TACR1
CC   segment is useful for analysing a nucleic acid, by obtaining the nucleic
CC   acid from an individual, and determining the base occupying any one of
CC   the polymorphic sites in the segment. The nucleic acid is obtained from
CC   several individuals, and the base occupying one of the polymorphic sites
CC   is determined in each of the individuals, and further involves testing
CC   each of the individuals for the presence of a disease phenotype, and
CC   correlating the presence with the base. The TACR1 segment is useful for
CC   diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
CC   The TACR1 segment is also useful in forensics, paternity testing,
CC   correlating polymorphisms with phenotypic traits, and genetic mapping of
CC   phenotypic traits. The TACR1 segment is useful in diagnosing and
CC   monitoring of diseases such as cancer, inflammation, heart disease,
CC   diseases of central nervous system, and susceptibility to infection to
CC   microorganisms. The TACR1 segment is also useful in the manufacture of a
CC   medicament for the treatment of the diseases. This polynucleotide
CC   sequence represents a polymorphic region of the human neurokinin 1
CC   receptor (TACR1) gene of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 60;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              |||||| |||
Db         10 AAGCCATACT 1


Search completed: April 15, 2004, 16:35:36
Job time : 1 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:36:47 ; Search time 0.001 Seconds
(without alignments)
34.620 Million cell updates/sec

Title: us-09-954-556-3
Perfect score: 30
Sequence: 1 cacgaccaagaagccagacttcagcagcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 44 seqs, 577 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 44 summaries

Database : rni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.4	48.0	17	1	US-08-541-950B-17	Sequence 17, Appl
2	14.4	48.0	17	1	US-08-541-950B-20	Sequence 20, Appl
3	14.4	48.0	17	1	US-09-083-756A-17	Sequence 17, Appl
4	14.4	48.0	17	1	US-09-083-756A-20	Sequence 20, Appl
5	14.4	48.0	18	1	US-08-541-950B-23	Sequence 23, Appl
6	14.4	48.0	18	1	US-09-083-756A-23	Sequence 23, Appl
7	13.8	46.0	17	1	US-09-325-601-1	Sequence 1, Appli
8	13.8	46.0	18	1	US-08-541-950B-13	Sequence 13, Appl
9	13.8	46.0	18	1	US-09-083-756A-13	Sequence 13, Appl
10	13.8	46.0	18	1	US-09-325-601-3	Sequence 3, Appli
11	12.8	42.7	17	1	US-08-541-950B-18	Sequence 18, Appl
12	12.8	42.7	17	1	US-08-541-950B-19	Sequence 19, Appl
13	12.8	42.7	17	1	US-08-541-950B-21	Sequence 21, Appl
14	12.8	42.7	17	1	US-08-541-950B-22	Sequence 22, Appl
15	12.8	42.7	17	1	US-09-083-756A-18	Sequence 18, Appl
16	12.8	42.7	17	1	US-09-083-756A-19	Sequence 19, Appl
17	12.8	42.7	17	1	US-09-083-756A-21	Sequence 21, Appl
18	12.8	42.7	17	1	US-09-083-756A-22	Sequence 22, Appl
c 19	11.8	39.3	15	1	US-08-363-240A-47	Sequence 47, Appl
c 20	11.4	38.0	15	1	US-08-050-073-65	Sequence 65, Appl
c 21	9.4	31.3	12	1	US-09-281-418-65	Sequence 65, Appl
c 22	9	30.0	10	1	US-09-508-753B-25	Sequence 25, Appl
23	8.4	28.0	10	1	US-09-263-790-36	Sequence 36, Appl
24	8.4	28.0	10	1	US-09-721-777-18	Sequence 18, Appl
25	8.4	28.0	10	1	US-08-545-253A-20	Sequence 20, Appl
26	8.4	28.0	10	1	US-08-719-337-20	Sequence 20, Appl
27	8.4	28.0	10	1	US-09-255-432-6	Sequence 6, Appli
c 28	8.4	28.0	10	1	US-08-878-835A-12	Sequence 12, Appl
29	8.4	28.0	10	1	US-09-508-753B-28	Sequence 28, Appl
c 30	8.4	28.0	10	1	US-09-508-753B-63	Sequence 63, Appl
31	8.4	28.0	10	1	US-08-894-454-110	Sequence 110, App
32	8.4	28.0	10	1	US-09-758-073-6	Sequence 6, Appli
c 33	8.4	28.0	11	1	US-08-173-489C-342	Sequence 342, App
c 34	8.4	28.0	11	1	US-09-862-847-15	Sequence 15, Appl
c 35	8	26.7	8	1	US-08-859-954-95	Sequence 95, Appl
c 36	8	26.7	8	1	US-09-041-675-19	Sequence 19, Appl
c 37	8	26.7	8	1	US-09-041-675-24	Sequence 24, Appl
c 38	8	26.7	9	1	US-09-989-789-455	Sequence 455, App
c 39	8	26.7	9	1	US-09-989-789-456	Sequence 456, App
c 40	8	26.7	10	1	US-08-060-952C-9	Sequence 9, Appli
41	8	26.7	10	1	US-08-997-897-4	Sequence 4, Appli
42	8	26.7	10	1	US-09-156-836B-4	Sequence 4, Appli
c 43	8	26.7	10	1	US-08-464-011B-9	Sequence 9, Appli
44	8	26.7	10	1	US-09-336-946B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-541-950B-17
; Sequence 17, Application US/08541950B
; Patent No. 5821046
; GENERAL INFORMATION:
; APPLICANT: Karn J, Gait MJ, Heaphy S, Dingwall C
; TITLE OF INVENTION: VIRAL (HIV) GROWTH INHIBITION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center, 45th Floor
; CITY: Boston
; STATE: MA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,950B
; FILING DATE: 10/10/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/960,370
; FILING DATE: 03/19/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3777/57347 (MRC-O11AX)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic RNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: N is 2'-deoxythymidine
US-08-541-950B-17

Query Match 48.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.9;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17
```

RESULT 2
US-08-541-950B-20
; Sequence 20, Application US/08541950B

```
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  8
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-08-541-950B-20

  Query Match             48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 2.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17


RESULT 3
US-09-083-756A-17
; Sequence 17, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  8
;      OTHER INFORMATION:  N is 2'-deoxythymidine
US-09-083-756A-17

  Query Match             48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 2.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17


RESULT 4
US-09-083-756A-20
; Sequence 20, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
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;      LOCATION:  8
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-09-083-756A-20

  Query Match             48.0%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 2.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17


RESULT 5
US-08-541-950B-23
; Sequence 23, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  8
;      OTHER INFORMATION:  N is 4-thio-2'-deoxythymidine
US-08-541-950B-23

  Query Match             48.0%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 3.1;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17


RESULT 6
US-09-083-756A-23
; Sequence 23, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  8
;      OTHER INFORMATION:  N is 4-thio-2'-deoxythymidine
US-09-083-756A-23

  Query Match             48.0%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 3.1;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGANUUGAGCAGC 17


RESULT 7
US-09-325-601-1
; Sequence 1, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
;  APPLICANT: Karn
;  APPLICANT: Prescott
;  TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
;  FILE REFERENCE: 3950/81235
;  CURRENT APPLICATION NUMBER: US/09/325,601
;  CURRENT FILING DATE: 1999-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Human immunodeficiency virus
US-09-325-601-1

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 3.7;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
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```
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 8
US-08-541-950B-13
; Sequence 13, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
US-08-541-950B-13

  Query Match           46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 3.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 9
US-09-083-756A-13
; Sequence 13, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-O11AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
US-09-083-756A-13

  Query Match           46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 3.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 10
US-09-325-601-3
; Sequence 3, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
;  APPLICANT: Karn
;  APPLICANT: Prescott
;  TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
;  FILE REFERENCE: 3950/81235
;  CURRENT APPLICATION NUMBER: US/09/325,601
;  CURRENT FILING DATE: 1999-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Human immunodeficiency virus
US-09-325-601-3

  Query Match           46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   76.5%;  Pred. No. 3.9;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :: ||||||
Db          1 AGCCAGAUUUGAGCAGC 17


RESULT 11
US-08-541-950B-18
; Sequence 18, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 6.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/541,950B
;       FILING DATE:  10/10/95
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/960,370
;       FILING DATE:  03/19/93
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Williams, Ph.D., Kathleen M.
;       REGISTRATION NUMBER:  34,380
;       REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 345-9100
;       TELEFAX:  (617) 345-9111
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  synthetic RNA
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  9
;       OTHER INFORMATION:  N is 2'-deoxythymidine
US-08-541-950B-18

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| : ||||||
Db          1 AGCCAGAUNUGAGCAGC 17


RESULT 12
US-08-541-950B-19
; Sequence 19, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  10
;      OTHER INFORMATION:  N is 2'-deoxythymidine
US-08-541-950B-19

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| : ||||||
Db          1 AGCCAGAUUNGAGCAGC 17


RESULT 13
US-08-541-950B-21
; Sequence 21, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  9
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-08-541-950B-21

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| : ||||||
Db          1 AGCCAGAUNUGAGCAGC 17
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```
RESULT 14
US-08-541-950B-22
; Sequence 22, Application US/08541950B
; Patent No. 5821046
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,950B
;      FILING DATE:  10/10/95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/960,370
;      FILING DATE:  03/19/93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  10
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-08-541-950B-22

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :  ||||||
Db          1 AGCCAGAUUNGAGCAGC 17


RESULT 15
US-09-083-756A-18
; Sequence 18, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  9
;      OTHER INFORMATION:  N is 2'-deoxythymidine
US-09-083-756A-18

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :  ||||||
Db          1 AGCCAGAUNUGAGCAGC 17


RESULT 16
US-09-083-756A-19
; Sequence 19, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  10
;      OTHER INFORMATION:  N is 2'-deoxythymidine
US-09-083-756A-19

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :  ||||||
Db          1 AGCCAGAUUNGAGCAGC 17


RESULT 17
US-09-083-756A-21
; Sequence 21, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  9
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-09-083-756A-21

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :  ||||||
Db          1 AGCCAGAUNUGAGCAGC 17


RESULT 18
US-09-083-756A-22
; Sequence 22, Application US/09083756A
; Patent No. 6114109
;  GENERAL INFORMATION:
;    APPLICANT:  Karn J, Gait MJ, Heaphy S, Dingwall C
;    TITLE OF INVENTION:  VIRAL (HIV) GROWTH INHIBITION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  One Financial Center, 45th Floor
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,756A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,950
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  3777/57347 (MRC-011AX)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic RNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  10
;      OTHER INFORMATION:  N is 5-bromo-2'-deoxyuridine
US-09-083-756A-22

  Query Match             42.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 5.6;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTTCAGCAGC 1506
              ||||||| :  ||||||
Db          1 AGCCAGAUUNGAGCAGC 17


RESULT 19
US-08-363-240A-47/c
; Sequence 47, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
```

```
;       ZIP:  90071
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/363,240A
;       FILING DATE:  December 23, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  210/096
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-363-240A-47

  Query Match             39.3%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 7.4;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTCAG 1502
                | ||||| |||||||
Db         15 GTAGCCATACTTCAG 1


RESULT 20
US-08-050-073-65/c
; Sequence 65, Application US/08050073
; Patent No. 5567809
;  GENERAL INFORMATION:
;     APPLICANT:  Apple, Raymond J.
;     APPLICANT:  Begovich, Ann B.
;     APPLICANT:  Bugawan, Teodorica L.
;     APPLICANT:  Erlich, Henry A.
;     APPLICANT:  Griffith, Robert L.
;     APPLICANT:  Scharf, Stephen J.
;     TITLE OF INVENTION:  Methods and Reagents for HLA DRBeta DNA
;     TITLE OF INVENTION:  Typing
;     NUMBER OF SEQUENCES:  315
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hoffmann-La Roche Inc.
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  U.S.A.
;       ZIP:  07110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/050,073
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petry, Douglas A.
;       REGISTRATION NUMBER:  35,321
;       REFERENCE/DOCKET NUMBER:  8769
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814-2974
;       TELEFAX:  (510) 814-2977
;   INFORMATION FOR SEQ ID NO:  65:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
US-08-050-073-65

  Query Match             33.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 8.7;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1494 AGACTTCAGCAGC 1506
                ||||||  ||||||
Db         15 AGACTTAAGCAGC 3


RESULT 21
US-09-281-418-65/c
; Sequence 65, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
;  APPLICANT: Inoue, Takakazu
;  TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fr
;  TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mic
;  TITLE OF INVENTION: nisms and Method of Assaying Contaminant
;  FILE REFERENCE: 9982-7
;  CURRENT APPLICATION NUMBER: US/09/281,418
;  CURRENT FILING DATE: 1999-03-30
;  EARLIER APPLICATION NUMBER: JP/1998/87651
;  EARLIER FILING DATE: 1998-03-31
;  EARLIER APPLICATION NUMBER: JP/1999/69694
;  EARLIER FILING DATE: 1999-03-16
;  NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 65
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-281-418-65

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                ||||||  ||||
Db         11 CCAAGAGGCCA 1


RESULT 22
US-09-508-753B-25/c
; Sequence 25, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 25
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```
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-25

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAG 1505
                |||||||||
Db         10 CTTCAGCAG 2


RESULT 23
US-09-263-790-36
; Sequence 36, Application US/09263790
; Patent No. PP12997
; GENERAL INFORMATION:
;  APPLICANT:  Nirmal Kumar PATRA et al.
;  TITLE OF INVENTION:   JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
;  FILE REFERENCE:   2761-0120P
;  CURRENT APPLICATION NUMBER: US/09/263,790
;  CURRENT FILING DATE:  1999-03-05
;  NUMBER OF SEQ ID NOS:   38
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: OPT 18 Primer - Used to develop the unique RAPD profiles of the
;   OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-36

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                || |||||||
Db          1 GATGCCAGAC 10


RESULT 24
US-09-721-777-18
; Sequence 18, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
;  APPLICANT: Khanuja, Suman Preet Singh
;  APPLICANT:  Kumar, Sushil
;  APPLICANT:  Shasany, Ajit Kumar
;  APPLICANT:  Dhawan, Sunita
;  APPLICANT:  Darokar, Mahendra Pandurang
;  APPLICANT:  Naqvi, Ali Arif
;  APPLICANT:  Dhawan, Om Parkash
;  APPLICANT:  Singh, Anil Kumar
;  APPLICANT:  Patra, Nirmal Kumar
;  APPLICANT:  Bahl, Janak Raj
;  APPLICANT:  Bansal, Ram Prakash
;  TITLE OF INVENTION: Mint Plant Named Saksham
;  FILE REFERENCE: 033166-002
;  CURRENT APPLICATION NUMBER: US/09/721,777
;  CURRENT FILING DATE:  2000-11-27
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: OPT primer
US-09-721-777-18

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                || |||||||
Db          1 GATGCCAGAC 10


RESULT 25
US-08-545-253A-20
; Sequence 20, Application US/08545253A
; Patent No. 5908978
;  GENERAL INFORMATION:
;    APPLICANT:  O'Malley, David M.
;    APPLICANT:  Sederoff, Ronald R.
;    APPLICANT:  Grattapaglia, Dario
;    APPLICANT:  Henry V. Amerson
;    APPLICANT:  Phillip Wilcox
;    APPLICANT:  E. George Kuhlman
;    TITLE OF INVENTION:  METHODS FOR WITHIN FAMILY
;    TITLE OF INVENTION:  SELECTION IN
;    TITLE OF INVENTION:  WOODY PERENNIALS USING GENETIC MARKERS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5908978th Carolina
;      COUNTRY:  U.S.A.
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,253A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5051-281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-545-253A-20

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                |||||||| |
Db          1 GAAGCCAGCC 10


RESULT 26
US-08-719-337-20
; Sequence 20, Application US/08719337
; Patent No. 6054634
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  O'Malley, David M.
;    APPLICANT:  Sederoff, Ronald R.
;    APPLICANT:  Grattapaglia, Dario
;    TITLE OF INVENTION:  METHODS FOR WITHIN FAMILY SELECTION IN
;    TITLE OF INVENTION:  WOODY PERENNIALS USING GENETIC MARKERS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 6054634th Carolina
;      COUNTRY:  U.S.A.
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/719,337
;      FILING DATE:  25-SEP-1996
;      CLASSIFICATION:  047
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/184,567
;      FILING DATE:  21-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5051-247
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-719-337-20

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                ||||||| |
Db          1 GAAGCCAGCC 10


RESULT 27
US-09-255-432-6
; Sequence 6, Application US/09255432
; Patent No. 6258537
;  GENERAL INFORMATION:
;    APPLICANT:  Keinath, et al.
;    TITLE OF INVENTION:  Method of Diagnosing Gummy Stem Blight in        Plants Usi
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Judy C. Jarecki-Black, Ph.D.
;      ADDRESSEE:  Dority & Manning, P.A.
;      STREET:  700 E. No. 6258537th Street, Suite 15
;      CITY:  Greenville
;      STATE:  South Carolina
;      COUNTRY:  USA
;      ZIP:  29601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS Dos; Windows 95
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/255,432
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:  Claims Priority to Provisional Application
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Judy C. Jarecki-Black, Ph.D.
;      REGISTRATION NUMBER:  P44,170
;      REFERENCE/DOCKET NUMBER:  CXU-291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (864) 271-1592
;      TELEFAX:  (864) 233-7342
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 Pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Other Nucleic Acid
;      DESCRIPTION:  Oligonucleotide Primer
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:  Operon Technologies (Alemeda, CA)
;    IMMEDIATE SOURCE:  Operon Technologies
;    POSITION IN GENOME:  No. 6258537 Applicable
;      UNITS:
;    FEATURE:
;      OTHER INFORMATION:  Commercially Available Primer
;    PUBLICATION INFORMATION:  No. 6258537 Applicable
US-09-255-432-6

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
                || |||||||
Db          1 GATGCCAGAC 10


RESULT 28
US-08-878-835A-12/c
; Sequence 12, Application US/08878835A
; Patent No. 6337071
;  GENERAL INFORMATION:
;    APPLICANT:  William Mitchell Molyneux
;    TITLE OF INVENTION:  Mosquito and/or Flea Control
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  D. Peter Hochberg Co., L.P.A.
;      STREET:  The Baker Building - Sixth Floor 1940 East 6th Street
;      STATE:  Ohio
;      COUNTRY:  U.S.A.
;      ZIP:  44114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MByte storage
;      COMPUTER:  IBM Compatible w/ Pentium Processor
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/878,835A
;      FILING DATE:  June 19, 1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PO 0605
;      FILING DATE:  21 June 1996
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
US-08-878-835A-12
```

```
  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAGCC 1507
              ||| ||||||
Db         10 TTCTGCAGCC 1

RESULT 29
US-09-508-753B-28
; Sequence 28, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 28
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-28

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCAG 1505
              || |||||||
Db          1 ACATCAGCAG 10

RESULT 30
US-09-508-753B-63/c
; Sequence 63, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 63
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-63

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCA 1504
              ||||||| ||
Db         10 GACTTCACCA 1

RESULT 31
US-08-894-454-110
; Sequence 110, Application US/08894454
; Patent No. 6544784
;  GENERAL INFORMATION:
;    APPLICANT:  VAN DEN VEN, W.J.M.
;    APPLICANT:  SCHOENMAKERS, H.F.P.M.
;    TITLE OF INVENTION:  MULTIPLE-TUMOR ABERRENT GROWTH
;    TITLE OF INVENTION:  GENES
;    NUMBER OF SEQUENCES:  164
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Webb Law Firm
;      STREET:  700 Koppers Building, 436 Seventh Avenue
;      CITY:  Pittsburgh
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  15219-1818
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,454
;      FILING DATE:  15-AUG-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP/00716
;      FILING DATE:  19-FEB-1996
;      APPLICATION NUMBER:  95200390.3
;      FILING DATE:  17-FEB-1995
;      APPLICATION NUMBER:  95201951.1
;      FILING DATE:  14-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Johnson, Barbara E
;      REGISTRATION NUMBER:  31,198
;      REFERENCE/DOCKET NUMBER:  702-971100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  412-471-8815
;      TELEFAX:  412-471-4094
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  110:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-894-454-110

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 20;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||||| |||
Db          1 AAGAAGGCAG 10

RESULT 32
US-09-758-073-6
; Sequence 6, Application US/09758073
; Patent No. 6610487
;  GENERAL INFORMATION:
;    APPLICANT:  Keinath, et al.
;    TITLE OF INVENTION:  Method of Diagnosing Gummy Stem Blight in
;    TITLE OF INVENTION:  Plants Using a Polymerase Chain Reaction Assay
```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Judy C. Jarecki-Black, Ph.D.
; ADDRESSEE: Dority & Manning, P.A.
; STREET: 700 E. No. 6610487th Street, Suite 15
; CITY: Greenville
; STATE: South Carolina
; COUNTRY: USA
; ZIP: 29601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS Dos; Windows 95
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,073
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/078,103
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy C. Jarecki-Black, Ph.D.
; REGISTRATION NUMBER: P44,170
; REFERENCE/DOCKET NUMBER: CXU-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (864) 271-1592
; TELEFAX: (864) 233-7342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other Nucleic Acid
; DESCRIPTION: Oligonucleotide Primer
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE: Operon Technologies (Alemeda, CA)
; IMMEDIATE SOURCE: Operon Technologies
; POSITION IN GENOME: No. 6610487 Applicable
; UNITS:
; FEATURE:
; OTHER INFORMATION: Commercially Available Primer
; PUBLICATION INFORMATION: No. 6610487 Applicable
US-09-758-073-6

Query Match 28.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1488 GAAGCCAGAC 1497
|| |||||||
Db 1 GATGCCAGAC 10

RESULT 33
US-08-173-489C-342/c
; Sequence 342, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 342:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from P. cepacea
; DESCRIPTION: 16s region in Seq ID No. 5861244341
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 342 :FROM 1 TO 11
US-08-173-489C-342

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1482 GACCAAGAAG 1491
|| |||||||
Db 11 GAACAAGAAG 2

RESULT 34
US-09-862-847-15/c
; Sequence 15, Application US/09862847
; Patent No. 6593111
; GENERAL INFORMATION:
; APPLICANT: Baric, Ralph S.
; APPLICANT: Boyd, Yount
; TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
; FILE REFERENCE: 5470.270
; CURRENT APPLICATION NUMBER: US/09/862,847
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/206,537
; PRIOR FILING DATE: 2000-05-21
; PRIOR APPLICATION NUMBER: US 60/285,320
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1484 CCAAGAAGCC 1493

```
              |||||||| |
Db          10 CCAAGAAGGC 1


RESULT 35
US-08-859-954-95/c
; Sequence 95, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-95

  Query Match             26.7%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGC 1503
              ||||||||
Db          8 ACTTCAGC 1


RESULT 36
US-09-041-675-19/c
; Sequence 19, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
;  APPLICANT: Kern, Scott
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Dai, Jia Le
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human SMAD3 and SMAD4 are
;  TITLE OF INVENTION: sequence-specific transcription activators
;  FILE REFERENCE: 01107.74098
;  CURRENT APPLICATION NUMBER: US/09/041,675A
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic random oligonucleotides selected for
;   OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-19

  Query Match             26.7%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGAC 1497
              ||||||||
Db          8 AGCCAGAC 1


RESULT 37
US-09-041-675-24/c
; Sequence 24, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
;  APPLICANT: Kern, Scott
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Dai, Jia Le
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human SMAD3 and SMAD4 are
;  TITLE OF INVENTION: sequence-specific transcription activators
;  FILE REFERENCE: 01107.74098
;  CURRENT APPLICATION NUMBER: US/09/041,675A
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic random oligonucleotides selected for
;   OTHER INFORMATION: binding to human SMAD3 or human SMAD4
US-09-041-675-24

  Query Match             26.7%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGAC 1497
              ||||||||
Db          8 AGCCAGAC 1


RESULT 38
US-09-989-789-455/c
; Sequence 455, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
```

```
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-455

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 39
US-09-989-789-456/c
; Sequence 456, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 456
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-456

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 40
US-08-060-952C-9/c
; Sequence 9, Application US/08060952C
; Patent No. 5695932
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/060,952C
;      FILING DATE:  May 13, 1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-060-952C-9

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1483 ACCAAGAA 1490
                ||||||||
Db          8 ACCAAGAA 1


RESULT 41
US-08-997-897-4
; Sequence 4, Application US/08997897C
; Patent No. 6114514
; GENERAL INFORMATION:
;  APPLICANT: SRIVASTAVA, RANJANA
;  APPLICANT: KUMAR, DEEPAK
;  APPLICANT: SRIVASTAVA, BRAHM SHANKER
;  TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
;  FILE REFERENCE: u011469-7
;  CURRENT APPLICATION NUMBER: US/08/997,897C
;  CURRENT FILING DATE: 1997-12-24
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-08-997-897-4

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCC 1493
                ||||||||
Db          3 AAGAAGCC 10


RESULT 42
US-09-156-836B-4
; Sequence 4, Application US/09156836B
; Patent No. 6242585
; GENERAL INFORMATION:
;  APPLICANT:  Srivastava, Ranjana
;  APPLICANT:  Kumar, Deepak
;  APPLICANT:  Srivastava, Brahm Shanker
```

```
;  TITLE OF INVENTION:  MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
;  FILE REFERENCE:  U 011876-4
;  CURRENT APPLICATION NUMBER: US/09/156,836B
;  CURRENT FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  08/997,897
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  7
; .SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-156-836B-4

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCC 1493
              ||||||||
Db          3 AAGAAGCC 10


RESULT 43
US-08-464-011B-9/c
; Sequence 9, Application US/08464011B
; Patent No. 6368789
;   GENERAL INFORMATION:
;        APPLICANT: Michael D. West
;                   Jerry W. Shay
;                   Woodring E. Wright
;        TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
;                            RELATED TO TELOMERE LENGTH AND/OR
;                            TELOMERASE ACTIVITY
;        NUMBER OF SEQUENCES: 61
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: Word Perfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,011B
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 07/882,438
;             FILING DATE: May 13, 1992
;             APPLICATION NUMBER: 08/038,766
;             FILING DATE: March 24, 1993
;             APPLICATION NUMBER: 08/060,952
;             FILING DATE: May 13, 1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 202/045
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-464-011B-9

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1483 ACCAAGAA 1490
              ||||||||
Db          8 ACCAAGAA 1


RESULT 44
US-09-336-946B-15
; Sequence 15, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
;  APPLICANT: Valent, Barbara S.
;  APPLICANT:  Bryan, Gregory
;  APPLICANT:  E. I. du Pont de Nemours and Company
;  TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
;  FILE REFERENCE: BB-1136
;  CURRENT APPLICATION NUMBER: US/09/336,946B
;  CURRENT FILING DATE:  1999-06-21
;  PRIOR APPLICATION NUMBER: 60/095229
;  PRIOR FILING DATE: 1998-08-04
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic oligonucleotide
US-09-336-946B-15

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGAC 1497
              ||||||||
Db          2 AGCCAGAC 9


Search completed: April 15, 2004, 16:36:47
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:38:43 ; Search time 0.001 Seconds
(without alignments)
30.420 Million cell updates/sec

Title: us-09-954-556-3
Perfect score: 30
Sequence: 1 cacgaccaagaagccagacttcagcagcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 43 seqs, 507 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 44 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20	66.7	20	1	US-09-954-556-65	Sequence 65, Appl
c	2	20	66.7	20	1	US-09-954-556-66	Sequence 66, Appl
c	3	20	66.7	20	1	US-09-954-556-67	Sequence 67, Appl
	4	13.8	46.0	17	1	US-10-307-005-1799	Sequence 1799, Ap
c	5	13.8	46.0	17	1	US-10-307-005-1800	Sequence 1800, Ap
	6	13.8	46.0	18	1	US-10-004-551-40	Sequence 40, Appl
c	7	13.8	46.0	18	1	US-10-004-551-43	Sequence 43, Appl
c	8	12	40.0	14	1	US-09-504-231A-1451	Sequence 1451, Ap
c	9	12	40.0	14	1	US-09-274-553D-1451	Sequence 1451, Ap
c	10	10.8	36.0	14	1	US-09-504-231A-1435	Sequence 1435, Ap
c	11	10.8	36.0	14	1	US-09-274-553D-1435	Sequence 1435, Ap
	12	10	33.3	10	1	US-10-033-145-1327	Sequence 1327, Ap
	13	10	33.3	13	1	US-09-823-887C-17	Sequence 17, Appl
	14	10	33.3	13	1	US-10-106-799-13	Sequence 13, Appl
c	15	9.4	31.3	12	1	US-10-240-580-10	Sequence 10, Appl
	16	9	30.0	10	1	US-08-935-377-14	Sequence 14, Appl
	17	9	30.0	10	1	US-09-822-250-14	Sequence 14, Appl
c	18	9	30.0	10	1	US-10-033-145-1647	Sequence 1647, Ap
c	19	9	30.0	10	1	US-10-044-674-86	Sequence 86, Appl
	20	8.4	28.0	10	1	US-09-758-073-6	Sequence 6, Appli
c	21	8.4	28.0	10	1	US-09-772-105-77	Sequence 77, Appl
	22	8.4	28.0	10	1	US-10-033-145-1651	Sequence 1651, Ap
c	23	8.4	28.0	10	1	US-10-330-627-141	Sequence 141, App
	24	8.4	28.0	10	1	US-10-330-627-292	Sequence 292, App
c	25	8.4	28.0	10	1	US-10-330-627-1077	Sequence 1077, Ap
	26	8.4	28.0	10	1	US-10-352-615-110	Sequence 110, App
c	27	8.4	28.0	11	1	US-09-862-847-15	Sequence 15, Appl
c	28	8.4	28.0	11	1	US-10-146-354A-16	Sequence 16, Appl
	29	8.2	27.3	20	1	US-09-954-556-66	Sequence 66, Appl
c	30	8	26.7	9	1	US-09-989-789-455	Sequence 455, App
c	31	8	26.7	9	1	US-09-989-789-456	Sequence 456, App
c	32	8	26.7	9	1	US-09-990-186-455	Sequence 455, App
c	33	8	26.7	9	1	US-09-990-186-456	Sequence 456, App
c	34	8	26.7	9	1	US-09-989-994-455	Sequence 455, App
c	35	8	26.7	9	1	US-09-989-994-456	Sequence 456, App
	36	8	26.7	9	1	US-10-113-877-5	Sequence 5, Appli
	37	8	26.7	9	1	US-10-339-161-6	Sequence 6, Appli
c	38	8	26.7	9	1	US-10-277-494-147	Sequence 147, App
c	39	8	26.7	10	1	US-08-463-404-9	Sequence 9, Appli
c	40	8	26.7	10	1	US-10-033-145-185	Sequence 185, App
	41	8	26.7	10	1	US-10-033-145-1011	Sequence 1011, Ap
c	42	8	26.7	10	1	US-10-113-030-3	Sequence 3, Appli
c	43	8	26.7	10	1	US-10-358-818-3	Sequence 3, Appli
c	44	8	26.7	10	1	US-10-330-627-344	Sequence 344, App

ALIGNMENTS

RESULT 1
US-09-954-556-65/c
; Sequence 65, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-65

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1479 CACGACCAAGAAGCCAGACT 1498
              ||||||||||||||||||||
Db         20 CACGACCAAGAAGCCAGACT 1
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RESULT 2
US-09-954-556-66/c
; Sequence 66, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-66

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1484 CCAAGAAGCCAGACTTCAGC 1503
              ||||||||||||||||||||
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Db         20 CCAAGAAGCCAGACTTCAGC 1


RESULT 3
US-09-954-556-67/c
; Sequence 67, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Scott Cooper
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
;  FILE REFERENCE: RTS-0250
;  CURRENT APPLICATION NUMBER: US/09/954,556
;  CURRENT FILING DATE:  2001-09-14
;  NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-67

  Query Match             66.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACTTCAGCAGCCA 1508
             ||||||||||||||||||||
Db         20 AAGCCAGACTTCAGCAGCCA 1


RESULT 4
US-10-307-005-1799
; Sequence 1799, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
;  APPLICANT: University of Delaware
;  APPLICANT:  Eric B. Kmiec
;  APPLICANT:  Howard B. Gamper
;  APPLICANT:  Michael C. Rice
;  APPLICANT:  Jungsup Kim
;  TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
;  TITLE OF INVENTION:  Using Modified Single Stranded Oligonucleotides
;  FILE REFERENCE: Napro/009 PCT
;  CURRENT APPLICATION NUMBER: US/10/307,005
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: PCT/US01/17672
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: US 60/208,538
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: US 60/244,989
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/818,875
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 2717
;  SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1799
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Solanum tuberosum
US-10-307-005-1799

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.8;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAGACTTCA 1501
             ||||||||  | ||||||
Db          1 CAAGAAGCTAAACTTCA 17


RESULT 5
US-10-307-005-1800/c
; Sequence 1800, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
;  APPLICANT: University of Delaware
;  APPLICANT:  Eric B. Kmiec
;  APPLICANT:  Howard B. Gamper
;  APPLICANT:  Michael C. Rice
;  APPLICANT:  Jungsup Kim
;  TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
;  TITLE OF INVENTION:  Using Modified Single Stranded Oligonucleotides
;  FILE REFERENCE: Napro/009 PCT
;  CURRENT APPLICATION NUMBER: US/10/307,005
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: PCT/US01/17672
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: US 60/208,538
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: US 60/244,989
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/818,875
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 2717
;  SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1800
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Solanum tuberosum
US-10-307-005-1800

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 4.8;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCAGACTTCA 1501
             ||||||||  | ||||||
Db          17 CAAGAAGCTAAACTTCA 1


RESULT 6
US-10-004-551-40
; Sequence 40, Application US/10004551
; Publication No. US20030004310A1
; GENERAL INFORMATION:
;  APPLICANT: SHIMKETS, RICHARD A
;  APPLICANT:  FERNANDES, ELMA
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;  FILE REFERENCE: 15965-559
;  CURRENT APPLICATION NUMBER: US/10/004,551
;  CURRENT FILING DATE:  2001-12-05
;  PRIOR APPLICATION NUMBER: 09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-10-004-551-40

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 5.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
             | ||||||||||||| |
Db          2 CTACCAAGAAGCCAGCC 18


RESULT 7
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US-10-004-551-43/c
; Sequence 43, Application US/10004551
; Publication No. US20030004310A1
; GENERAL INFORMATION:
;  APPLICANT: SHIMKETS, RICHARD A
;  APPLICANT:  FERNANDES, ELMA
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;  FILE REFERENCE: 15966-559
;  CURRENT APPLICATION NUMBER: US/10/004,551
;  CURRENT FILING DATE:  2001-12-05
;  PRIOR APPLICATION NUMBER: 09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-10-004-551-43

  Query Match             46.0%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 5.1;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1481 CGACCAAGAAGCCAGAC 1497
                | ||||||||||||| |
Db         17 CTACCAAGAAGCCAGCC 1


RESULT 8
US-09-504-231A-1451/c
; Sequence 1451, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1451
;   LENGTH: 14
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-1451

  Query Match             40.0%;  Score 12;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGCCA 1508
                ||||||||||||
Db         12 CTTCAGCAGCCA 1


RESULT 9
US-09-274-553D-1451/c
; Sequence 1451, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1451
;   LENGTH: 14
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-274-553D-1451

  Query Match             40.0%;  Score 12;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGCCA 1508
                ||||||||||||
Db         12 CTTCAGCAGCCA 1


RESULT 10
US-09-504-231A-1435/c
; Sequence 1435, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1435
;   LENGTH: 14
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-1435
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  Query Match            36.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity  85.7%;  Pred. No. 11;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAGCCA 1508
              || || ||||||||
Db         14 GAGTTGAGCAGCCA 1


RESULT 11
US-09-274-553D-1435/c
; Sequence 1435, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1435
;   LENGTH: 14
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-274-553D-1435

  Query Match            36.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity  85.7%;  Pred. No. 11;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1495 GACTTCAGCAGCCA 1508
              || || ||||||||
Db         14 GAGTTGAGCAGCCA 1


RESULT 12
US-10-033-145-1327
; Sequence 1327, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1327
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1327

  Query Match            33.3%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1487 AGAAGCCAGA 1496
              ||||||||||
Db          1 AGAAGCCAGA 10


RESULT 13
US-09-823-887C-17
; Sequence 17, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Repr
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Kur
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-17

  Query Match            33.3%;  Score 10;  DB 1;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              ||||||||||
Db          4 CTTCAGCAGC 13


RESULT 14
US-10-106-799-13
; Sequence 13, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: AP34 arbitrary primer for differential display
US-10-106-799-13

  Query Match            33.3%;  Score 10;  DB 1;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1497 CTTCAGCAGC 1506
              ||||||||||
Db          4 CTTCAGCAGC 13


RESULT 15
US-10-240-580-10/c
; Sequence 10, Application US/10240580
; Publication No. US20030180716A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: INOUE, Takakazu
;  TITLE OF INVENTION: METHOD AND APPARATUS FOR MICROORGANISM DISCRIMINATION, METHOD OF
;  TITLE OF INVENTION:  DATABASE FOR MICROORGANISM DISCRIMINATION, AND MICROORGANISM DIS
;  TITLE OF INVENTION:  PROGRAM AND RECORDING MEDIUM ON WHICH SUCH PROGRAM IS RECORDED
;  FILE REFERENCE: 9982-24
;  CURRENT APPLICATION NUMBER: US/10/240,580
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: PCT/JP01/02516
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: JP 2000-99482
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-240-580-10

  Query Match             31.3%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 15;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCCA 1494
                 |||||| ||||
Db         11 CCAAGAGGCCA 1


RESULT 16
US-08-935-377-14
; Sequence 14, Application US/08935377
; Publication No. US20030133917A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zauderer, Maurice
;    TITLE OF INVENTION:  T Cells Specific for Target Antigens and
;    TITLE OF INVENTION:  Vaccines Based Thereon
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,377
;      FILING DATE:  22-SEP-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1821.0010000/EKS/CMB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-935-377-14

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
                 |||||||||
Db          2 CAGACTTCA 10


RESULT 17
US-09-822-250-14
; Sequence 14, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
;  APPLICANT: Zauderer, Maurice
;  TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
;  FILE REFERENCE: 1821.0010001
;  CURRENT APPLICATION NUMBER: US/09/822,250
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 08/935,377
;  PRIOR FILING DATE: 1997-09-22
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: synthetic construct
US-09-822-250-14

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTCA 1501
                 |||||||||
Db          2 CAGACTTCA 10


RESULT 18
US-10-033-145-1647/c
; Sequence 1647, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1647

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCCA 1508
                 |||||||||
Db         10 CAGCAGCCA 2


RESULT 19
US-10-044-674-86/c
; Sequence 86, Application US/10044674
; Publication No. US20030175710A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Chew, Anne
;  APPLICANT:  Denton, R. Rex
;  APPLICANT:  Bieglecki, Karyn M
;  APPLICANT:  Nandabalan, Krishnan
;  APPLICANT:  Stephens, J. Claiborne
;  TITLE OF INVENTION: HAPLOTYPES OF THE TNFRSF11B GENE
;  FILE REFERENCE: TNFRSF11B_MWH-0001US (CIP)
;  CURRENT APPLICATION NUMBER: US/10/044,674
;  CURRENT FILING DATE:  2002-01-09
;  PRIOR APPLICATION NUMBER: PCT/US00/18803
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-044-674-86

  Query Match             30.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCA 1504
             |||||||||
Db          9 ACTTCAGCA 1


RESULT 20
US-09-758-073-6
; Sequence 6, Application US/09758073
; Patent No. US20010024785A1
;  GENERAL INFORMATION:
;    APPLICANT:  Keinath, et al.
;    TITLE OF INVENTION:  Method of Diagnosing Gummy Stem Blight in
;    TITLE OF INVENTION:  Plants Using a Polymerase Chain Reaction Assay
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Judy C. Jarecki-Black, Ph.D.
;      ADDRESSEE:  Dority & Manning, P.A.
;      STREET:  700 E. No. US20010024785A1th Street, Suite 15
;      CITY:  Greenville
;      STATE:  South Carolina
;      COUNTRY:  USA
;      ZIP:  29601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS Dos; Windows 95
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/758,073
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/078,103
;      FILING DATE:  16-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Judy C. Jarecki-Black, Ph.D.
;      REGISTRATION NUMBER:  P44,170
;      REFERENCE/DOCKET NUMBER:  CXU-291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (864) 271-1592
;      TELEFAX:  (864) 233-7342
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 Pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Other Nucleic Acid
;      DESCRIPTION:  Oligonucleotide Primer
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:  Operon Technologies (Alemeda, CA)
;    IMMEDIATE SOURCE:  Operon Technologies
;    POSITION IN GENOME:  No. US20010024785A1 Applicable
;      UNITS:
;    FEATURE:
;      OTHER INFORMATION:  Commercially Available Primer
;    PUBLICATION INFORMATION:  No. US20010024785A1 Applicable
US-09-758-073-6

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
             || |||||||
Db          1 GATGCCAGAC 10


RESULT 21
US-09-772-105-77/c
; Sequence 77, Application US/09772105
; Patent No. US20010029015A1
; GENERAL INFORMATION:
;  APPLICANT:  Ozelius, Laurie J.
;  APPLICANT:  Breakefield, Xandra O.
;  TITLE OF INVENTION:  TORSIN, TORSIN-RELATED GENES, AND
;  TITLE OF INVENTION:  METHODS OF DETECTING NEURONAL DISEASES
;  FILE REFERENCE:  0838.1001009
;  CURRENT APPLICATION NUMBER: US/09/772,105
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER:  US 09/218,363
;  PRIOR FILING DATE:  1998-12-22
;  PRIOR APPLICATION NUMBER:  US 09/099,454
;  PRIOR FILING DATE:  1998-06-18
;  PRIOR APPLICATION NUMBER:  US 60/050,244
;  PRIOR FILING DATE:  1997-06-19
;  NUMBER OF SEQ ID NOS:  90
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Exon/intron of TORB
US-09-772-105-77

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1485 CAAGAAGCCA 1494
             | ||||||||
Db         10 CCAGAAGCCA 1


RESULT 22
US-10-033-145-1651
; Sequence 1651, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1651
```

```
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1651

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGAC 1497
              ||||||||| |
Db          1 GAAGCCAGCC 10


RESULT 23
US-10-330-627-141/c
; Sequence 141, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-141

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1496 ACTTCAGCAG 1505
              |||| |||||
Db         10 ACTTAAGCAG 1


RESULT 24
US-10-330-627-292
; Sequence 292, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-292

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1499 TCAGCAGCCA 1508
              ||| ||||||
Db          1 TCAACAGCCA 10


RESULT 25
US-10-330-627-1077/c
; Sequence 1077, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1077
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1077

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGACTT 1499
              |||||| |||
Db         10 AGCCAGTCTT 1


RESULT 26
US-10-352-615-110
; Sequence 110, Application US/10352615
; Publication No. US20030190285A1
;   GENERAL INFORMATION:
;        APPLICANT: VAN DEN VEN, W.J.M.
;                   SCHOENMAKERS, H.F.P.M.
;        TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
;                            GENES
;        NUMBER OF SEQUENCES: 164
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: The Webb Law Firm
;             STREET: 700 Koppers Building, 436 Seventh Avenue
;             CITY: Pittsburgh
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 15219-1818
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,615
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/894,454
;             FILING DATE: 15-AUG-1997
;             APPLICATION NUMBER: PCT/EP/00716
;             FILING DATE: 19-FEB-1996
;             APPLICATION NUMBER: 95200390.3
;             FILING DATE: 17-FEB-1995
;             APPLICATION NUMBER: 95201951.1
;             FILING DATE: 14-JUL-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Johnson, Barbara E
;             REGISTRATION NUMBER: 31,198
;             REFERENCE/DOCKET NUMBER: 702-971100
```

```
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 412-471-8815
;            TELEFAX: 412-471-4094
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 110:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-352-615-110

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1486 AAGAAGCCAG 1495
              |||||| |||
Db          1 AAGAAGGCAG 10


RESULT 27
US-09-862-847-15/c
; Sequence 15, Application US/09862847
; Patent No. US20020177230A1
; GENERAL INFORMATION:
;  APPLICANT: Baric, Ralph S.
;  APPLICANT:  Boyd, Yount
;  TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
;  FILE REFERENCE: 5470.270
;  CURRENT APPLICATION NUMBER: US/09/862,847
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/206,537
;  PRIOR FILING DATE: 2000-05-21
;  PRIOR APPLICATION NUMBER: US 60/285,320
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 19;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1484 CCAAGAAGCC 1493
              |||||||| |
Db         10 CCAAGAAGGC 1


RESULT 28
US-10-146-354A-16/c
; Sequence 16, Application US/10146354A
; Publication No. US20030054381A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Seymour, Albert B.
;  APPLICANT:  Nelson, Darcy L.
;  APPLICANT:  Webb, Suzin M.
;  APPLICANT:  Affourtit, Jason P.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
;  TITLE OF INVENTION:  USES IN DIAGNOSIS AND TREATMENT OF DISEASES
;  FILE REFERENCE: PC10461AGPR
;  CURRENT APPLICATION NUMBER: US/10/146,354A
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: 60/293,425
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-146-354A-16

  Query Match             28.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 19;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 AAGCCAGACT 1498
              |||||| |||
Db         10 AAGCCATACT 1


RESULT 29
US-09-954-556-66
; Sequence 66, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Scott Cooper
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES
;  FILE REFERENCE: RTS-0250
;  CURRENT APPLICATION NUMBER: US/09/954,556
;  CURRENT FILING DATE:  2001-09-14
;  NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 66
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-66

  Query Match             27.3%;  Score 8.2;  DB 1;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1488 GAAGCCAGACTTC 1500
              |||| | | ||||
Db          4 GAAGTCTGGCTTC 16


RESULT 30
US-09-989-789-455/c
; Sequence 455, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-455

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 31
US-09-989-789-456/c
; Sequence 456, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 456
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-456

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 32
US-09-990-186-455/c
; Sequence 455, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-455

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 33
US-09-990-186-456/c
; Sequence 456, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 456
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-456

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 34
US-09-989-994-455/c
; Sequence 455, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-455

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
                ||||||||
Db          8 CAGACTTC 1


RESULT 35
US-09-989-994-456/c
; Sequence 456, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,994
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 456
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-994-456

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1493 CAGACTTC 1500
              ||||||||
Db          8 CAGACTTC 1


RESULT 36
US-10-113-877-5
; Sequence 5, Application US/10113877
; Publication No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-5

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGAC 1497
              ||||||||
Db          1 AGCCAGAC 8


RESULT 37
US-10-339-161-6
; Sequence 6, Application US/10339161
; Publication No. US20030162211A1
; GENERAL INFORMATION:
;  APPLICANT: Remacle, Jose
;  APPLICANT:  Renard, Patricia
;  APPLICANT:  Art, Muriel
;  TITLE OF INVENTION: METHOD AND KIT FOR THE DETERMINATION OF
;  TITLE OF INVENTION:  CELLULAR ACTIVATION PROFILES
;  FILE REFERENCE: VANM212.001CP1
;  CURRENT APPLICATION NUMBER: US/10/339,161
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: US 09/816,763
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: EP 00870057.7
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Transcription factor SMAD 4
US-10-339-161-6

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1490 AGCCAGAC 1497
              ||||||||
Db          1 AGCCAGAC 8


RESULT 38
US-10-277-494-147/c
; Sequence 147, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Levels
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
;   LENGTH: 9
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-147

  Query Match             26.7%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCC 1507
              ||||||||
Db          8 CAGCAGCC 1


RESULT 39
US-08-463-404-9/c
; Sequence 9, Application US/08463404
; Publication No. US20020127634A1
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. West
;    APPLICANT:  Jerry W. Shay
;    APPLICANT:  Woodring E. Wright
;    APPLICANT:  Elizabeth Blackburn
;    TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF CONDITIONS
;    TITLE OF INVENTION:  RELATED TO TELOMERE LENGTH AND/OR
;    TITLE OF INVENTION:  TELOMERASE ACTIVITY
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,404
;      FILING DATE:  05-JUN-1995
```

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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/060,952
;      FILING DATE:  May 13, 1993
;      APPLICATION NUMBER:  07/882,438
;      FILING DATE:  May 13, 1992
;      APPLICATION NUMBER:  08/038,766
;      FILING DATE:  March 24, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  202/045
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-404-9

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1483 ACCAAGAA 1490
             ||||||||
Db          8 ACCAAGAA 1


RESULT 40
US-10-033-145-185/c
; Sequence 185, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 185
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-185

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1491 GCCAGACT 1498
             ||||||||
Db         10 GCCAGACT 3


RESULT 41
US-10-033-145-1011
; Sequence 1011, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1011
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1011

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1498 TTCAGCAG 1505
             ||||||||
Db          1 TTCAGCAG 8


RESULT 42
US-10-113-030-3/c
; Sequence 3, Application US/10113030
; Publication No. US20030077610A1
; GENERAL INFORMATION:
;  APPLICANT: Nelson, John
;  APPLICANT:  Fuller, Carl
;  APPLICANT:  Sood, Anup
;  APPLICANT:  Kumar, Shiv
;  TITLE OF INVENTION: Terminal-Phosphate-Labeled Nucleotides and Methods of Use
;  FILE REFERENCE: PB0156-1
;  CURRENT APPLICATION NUMBER: US/10/113,030
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: US 60/315,798
;  PRIOR FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Template
US-10-113-030-3

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCC 1507
             ||||||||
Db         10 CAGCAGCC 3


RESULT 43
US-10-358-818-3/c
; Sequence 3, Application US/10358818
; Publication No. US20030162213A1
; GENERAL INFORMATION:
;  APPLICANT: Fuller, Carl
;  APPLICANT:  Kumar, Shiv
;  APPLICANT:  Sood, Anup
;  APPLICANT:  Nelson, John
;  TITLE OF INVENTION: Terminal-Phosphate-Labeled Nucleotides and Methods of Use
;  FILE REFERENCE: PB0156-1CIP
;  CURRENT APPLICATION NUMBER: US/10/358,818
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US 60/315,798
;  PRIOR FILING DATE: 2001-08-29
;  PRIOR APPLICATION NUMBER: US 10/113,030
;  PRIOR FILING DATE: 2002-04-01
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;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA Template
US-10-358-818-3

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1500 CAGCAGCC 1507
              ||||||||
Db         10 CAGCAGCC 3


RESULT 44
US-10-330-627-344/c
; Sequence 344, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 344
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-344

  Query Match             26.7%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1501 AGCAGCCA 1508
              ||||||||
Db         10 AGCAGCCA 3


Search completed: April 15, 2004, 16:38:43
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:45:10 ; Search time 0.001 Seconds
(without alignments)
0.660 Million cell updates/sec

Title: us-09-954-556-3
Perfect score: 30
Sequence: 1 cacgaccaagaagccagacttcagcagcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 11 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rst.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8.4	28.0	11	1	BG896271	ACCESSION:BG896271

ALIGNMENTS

RESULT 1
BG896271
LOCUS BG896271 11 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA28-1-G6 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.
ACCESSION BG896271
VERSION BG896271.1 GI:14306512
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

Query Match 28.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1489 AAGCCAGACT 1498
              |||||||||
Db          1 ACGCCAGACT 10
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Search completed: April 15, 2004, 16:45:10
Job time : 0.001 secs